

GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 12, 2006, 02:04:54 ; Search time 25.404 Seconds
(without alignments)
1503.623 Million cell updates/sec

Title: US-10-668-936-17
Perfect score: 2131
Sequence: 1 MGLSWSRPPLMLLVLS.....PRLPILSILPLILLQLTW 397

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80.*
1: PIR1.*
2: PIR2.*
3: PIR3.*
4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2131	100.0	397	2 JE0082	GPI-linked recepto
2	132	6.2	4544	1 S02392	alpha-2-macroglobu
3	131	6.1	4545	1 S25111	alpha-2-macroglobu
4	124	5.8	1722	2 E89753	protein Filc7.4 [1
5	123	5.8	1964	2 T09059	notch4 - mouse
6	120.5	5.7	2531	2 A46019	notch-1 protein -
7	118	5.5	2555	2 A40043	notch protein homo
8	117	5.5	1746	1 S19694	tenascin precursor
9	117	5.5	4543	1 A53102	alpha-2-macroglobu
10	114.5	5.4	2531	2 S18188	notch protein homo
11	114	5.3	2437	2 S42612	transmembrane prot
12	112.5	5.3	2703	1 A24420	notch protein - fr
13	110	5.2	965	2 S62935	hypothetical prote
14	110	5.2	1187	2 T18355	hypothetical prote
15	110	5.2	2321	2 S78549	notch3 protein - h
16	109.5	5.1	2233	2 T28669	surface protein 51
17	109	5.1	1047	2 D71302	probable exonuclea
18	108	5.1	1394	2 A35626	transforming growt
19	108	5.1	1712	2 A38261	masking protein pr
20	108	5.1	1847	2 T18308	probable vitelloge
21	107.5	5.0	996	2 JE0237	apolipoprotein E r
22	107.5	5.0	2150	2 T32497	hypothetical prote
23	107	5.0	3051	2 S42373	hypothetical prote
24	106.5	5.0	2019	1 JQ1322	tenascin precursor
25	106	5.0	2918	2 A54105	fibillin-2 precur
26	105.5	5.0	384	2 S25771	gas1 protein - mou
27	105.5	5.0	873	1 A49729	VDL receptor prec
28	105	4.9	1077	2 T41146	probable cysteine-
29	105	4.9	1106	2 T13938	gene shuttle craft

30	105	4.9	1408	2 S16148	gene serrate prote
31	104.5	4.9	1203	2 A49175	Notch B protein -
32	103.5	4.9	869	1 JC4858	VDL receptor prec
33	103	4.8	886	2 A57172	probable hormone r
34	103	4.8	2318	2 S45306	notch 3 protein -
35	102.5	4.8	835	2 JP0076	nel protein - chic
36	102.5	4.8	1188	2 D86236	jagged protein pre
37	102	4.8	1220	2 A56136	granulin precursor
38	101.5	4.8	593	1 GYHU	zonadhesin - mouse
39	100.5	4.7	5376	2 T42215	C-Delta-1 - chicke
40	100	4.7	728	2 I50719	hypothetical prote
41	100	4.7	1106	2 T44598	cell-fate determin
42	99.5	4.7	2471	2 A49128	G surface protein
43	99.5	4.7	2718	2 A23475	G surface protein
44	99	4.6	2704	2 S09118	fibillin-2 precur
45	99	4.6	2907	2 A57278	

ALIGNMENTS

RESULT 1
JE0082
GPI-linked receptor precursor - mouse
N:Alternate names: GFRalpha-3
C:Species: Mus musculus (house mouse)
C>Date: 21-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
C:Accession: JE0082
R:Nomoto, S.; Ito, S.; Yang, L.X.; Kiuchi, K.
Biochem. Biophys. Res. Commun. 244, 849-853, 1998
A:Title: Molecular cloning and expression analysis of GFRalpha-3, a novel cDNA related t
A:Reference number: JE0082; MUID:98205811; PMID:9535755
A:Accession: JE0082
A:Molecule type: mRNA
A:Residues: 1-397 <NOM>
A:Cross-references: UNIPROT:O35118; UNIPARC:UPI0000002231A; DBJ:AB008833; NID:92627159;
C:Comment: This protein plays a distinct role in cell survival and differentiation.
C:Superfamily: Mus musculus GPI-linked receptor
C:Keywords: glycoprotein
F:1-25/Domain: signal sequence #status predicted <SIG>
F:380-397/Region: hydrophobic
F:92,145,306/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match	100.0%;	Score 2131;	DB 2;	Length 397;
Best Local Similarity	100.0%;	Pred. No. 8.2e-166;		
Matches	397;	Conservative 0;	Mismatches 0;	Indels 0; Gaps 0;
Qy	1	MGLSWSRPPLMLLVLSIMLPLGAGNSLATENRFVNSCTQARKKCEANPACKAAYQH	60	
Db	1	MGLSWSRPPLMLLVLSIMLPLGAGNSLATENRFVNSCTQARKKCEANPACKAAYQH	60	
Qy	61	LGSTCTSLSRPLPLEESAMSDCLAEAEQLRNSLIDCRCHRRMKHOATCLDIYVTVHPA	120	
Db	61	LGSTCTSLSRPLPLEESAMSDCLAEAEQLRNSLIDCRCHRRMKHOATCLDIYVTVHPA	120	
Qy	121	RLSGDYELDVSPYEDVTTSKPKWNLSKLNKLKPDSDCLCKFAMLCCTLHKDCDLRKAYG	180	
Db	121	RLSGDYELDVSPYEDVTTSKPKWNLSKLNKLKPDSDCLCKFAMLCCTLHKDCDLRKAYG	180	
Qy	181	EACSGIRCQHLCLAQLRSFFEKAAESHAOGLLLCPCAPEDAGGERRNTIAPSCALPS	240	
Db	181	EACSGIRCQHLCLAQLRSFFEKAAESHAOGLLLCPCAPEDAGGERRNTIAPSCALPS	240	
Qy	241	VTNCLDLRSFCRADPLCRSLMDPOTHCHPMDILGTTCATEQSCLRAYLGLICTATPN	300	
Db	241	VTNCLDLRSFCRADPLCRSLMDPOTHCHPMDILGTTCATEQSCLRAYLGLICTATPN	300	
Qy	301	FISKVNTVALSCTCRSGNLDQCEQLERSFSQNPCLVEAIAAKMFHRLFSQDWADS	360	
Db	301	FISKVNTVALSCTCRSGNLDQCEQLERSFSQNPCLVEAIAAKMFHRLFSQDWADS	360	
Qy	361	TFSVVQOQNSNPALRQPLPILSILPILLQLTW	397	

Db 361 TFSVQQNSPALRQLPRLPIILSFILPLLQLTL 397

RESULT 2

alpha-2-macroglobulin receptor precursor - human

N;Alternate names: CD91; LDL receptor-related protein 1; low density lipoprotein receptor

C;Species: Homo sapiens (man)

C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 09-Jul-2004

C;Accession: S02392; S30027; I37998; A39210; S12538

R;Herz, J.; Hamann, U.; Rognie, S.; Myklebost, O.; Gausepohl, H.; Stanley, K.K.

EMBO J. 7, 4119-4127, 1988

A;Title: Surface location and high affinity for calcium of a 500-kd liver membrane protein

A;Reference number: S02392; MUID:89210795; PMID:3266596

A;Accession: S02392

A;Status: nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 1-4544 <HER>

A;Cross-references: UNIPROT:Q07954; UNIPARC:UPI0000055B03; EMBL:X13916; NID:g34338; PIDN submitted to the EMBL Data Library, October 1990

A;Reference number: S30027

A;Accession: S30027

A;Molecule type: mRNA

A;Residues: 3275-3864 <KRI>

A;Cross-references: UNIPARC:UPI00001736CD; EMBL:X55077

R;Herz, J.; Kowal, R.C.; Goldstein, J.L.; Brown, M.S.

EMBO J. 9, 1769-1776, 1990

A;Title: Proteolytic processing of the 600 kd low density lipoprotein receptor-related protein

A;Reference number: S12538; MUID:90269210; PMID:2112085

A;Contents: annotation; site of proteolytic cleavage

R;Kutt, H.; Herz, J.; Stanley, K.K.

Biochem. Biophys. Acta 1009, 229-236, 1989

A;Title: Structure of the low-density lipoprotein receptor-related protein (LRP) promotes

A;Reference number: I37998; MUID:90089395; PMID:2597675

A;Accession: I37998

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-11 <RES>

A;Cross-references: UNIPARC:UPI0000000A1E; EMBL:X15424; NID:g34408; PIDN:CAA333464.1; PID R;Strickland, D.K.; Ashcom, J.D.; Williams, S.; Burgess, W.H.; Miglierini, M.; Arggraves, J. Biol. Chem. 265, 17401-17404, 1990

A;Title: Sequence identity between the alpha2-macroglobulin receptor and low density lip

A;Reference number: A39210; MUID:91009181; PMID:1698775

A;Accession: A39210

A;Status: preliminary

A;Molecule type: protein

A;Residues: 150-166;234-238, 'X', 240-245, 'X', 247-252, 'G', 686-695;902-916;1096-1109; 'S', 17

A;Cross-references: UNIPARC:UPI00001736CB; UNIPARC:UPI00001736CF; UNIPARC:UPI00001736D0; 6D5; UNIPARC:UPI00001736D6; UNIPARC:UPI00001736D7

C;Genetics:

A;Gene: GDB:LRP1; APR; LRP; A2MR

A;Cross-references: GDB:119694; OMIM:107770

A;Map position: 12q13.1-12q13.3

C;Complex: The alpha-2-macroglobulin receptor complex consists of noncovalently-associated protein (see PIR:A39875).

C;Superfamily: alpha-2-macroglobulin receptor; EGF homology; LDL receptor ligand-binding

F;1-19/Domain: signal sequence #status predicted <SIG>

F;20-3943/Product: alpha-2-macroglobulin receptor 515K chain #status predicted <S15K>

F;27-64/Domain: LDL receptor ligand-binding repeat homology <LDL1>

F;72-108/Domain: LDL receptor ligand-binding repeat homology <LDL2>

F;115-148/Domain: EGF homology <EG1>

F;154-188/Domain: EGF homology <EG2>

F;198-239/Domain: LDL receptor WYTD-containing repeat homology <YW01>

F;240-281/Domain: LDL receptor WYTD-containing repeat homology <YW02>

F;292-334/Domain: LDL receptor WYTD-containing repeat homology <YW03>

F;335-378/Domain: LDL receptor WYTD-containing repeat homology <YW04>

F;379-420/Domain: LDL receptor WYTD-containing repeat homology <YW05>

F;421-468/Domain: LDL receptor WYTD-containing repeat homology <YW06>

F;478-519/Domain: EGF homology <EG3>

F;571-613/Domain: LDL receptor WYTD-containing repeat homology <YW07>

F;614-659/Domain: LDL receptor WYTD-containing repeat homology <YW08>

F;660-710/Domain: LDL receptor WYTD-containing repeat homology <YW09>

F;711-752/Domain: LDL receptor WYTD-containing repeat homology <YW10>

F;753-799/Domain: LDL receptor WYTD-containing repeat homology <YW11>

F;807-842/Domain: EGF homology <EG4>

F;854-890/Domain: LDL receptor ligand-binding repeat homology <LDL3>

F;895-931/Domain: LDL receptor ligand-binding repeat homology <LDL4>

F;936-971/Domain: LDL receptor ligand-binding repeat homology <LDL5>

F;976-1011/Domain: LDL receptor ligand-binding repeat homology <LDL6>

F;1015-1051/Domain: LDL receptor ligand-binding repeat homology <LDL7>

F;1062-1097/Domain: LDL receptor ligand-binding repeat homology <LDL8>

F;1104-1140/Domain: LDL receptor ligand-binding repeat homology <LDL9>

F;1145-1182/Domain: LDL receptor ligand-binding repeat homology <LDL10>

F;1185-1221/Domain: EGF homology <EG5>

F;1227-1261/Domain: EGF homology <EG6>

F;1269-1308/Domain: LDL receptor WYTD-containing repeat homology <YW12>

F;1309-1355/Domain: LDL receptor WYTD-containing repeat homology <YW13>

F;1356-1398/Domain: LDL receptor WYTD-containing repeat homology <YW14>

F;1399-1445/Domain: LDL receptor WYTD-containing repeat homology <YW15>

F;1446-1488/Domain: LDL receptor WYTD-containing repeat homology <YW16>

F;1489-1531/Domain: LDL receptor WYTD-containing repeat homology <YW17>

F;1540-1578/Domain: EGF homology <EG7>

F;1583-1626/Domain: LDL receptor WYTD-containing repeat homology <YW18>

F;1627-1669/Domain: LDL receptor WYTD-containing repeat homology <YW19>

F;1670-1713/Domain: LDL receptor WYTD-containing repeat homology <YW20>

F;1714-1753/Domain: LDL receptor WYTD-containing repeat homology <YW21>

F;1754-1796/Domain: LDL receptor WYTD-containing repeat homology <YW22>

F;1797-1846/Domain: LDL receptor WYTD-containing repeat homology <YW23>

F;1850-1886/Domain: EGF homology <EG8>

F;1934-1976/Domain: LDL receptor WYTD-containing repeat homology <YW24>

F;1977-2019/Domain: LDL receptor WYTD-containing repeat homology <YW25>

F;2020-2063/Domain: LDL receptor WYTD-containing repeat homology <YW26>

F;2064-2105/Domain: LDL receptor WYTD-containing repeat homology <YW27>

F;2106-2151/Domain: LDL receptor WYTD-containing repeat homology <YW28>

F;2159-2194/Domain: EGF homology <EG9>

F;2199-2241/Domain: LDL receptor WYTD-containing repeat homology <YW29>

F;2253-2294/Domain: LDL receptor WYTD-containing repeat homology <YW30>

F;2344-2388/Domain: LDL receptor WYTD-containing repeat homology <YW31>

F;2389-2429/Domain: LDL receptor WYTD-containing repeat homology <YW32>

F;2430-2473/Domain: LDL receptor WYTD-containing repeat homology <YW33>

F;2482-2517/Domain: EGF homology <EG10>

F;2524-2561/Domain: LDL receptor ligand-binding repeat homology <LDLB>

F;2566-2600/Domain: LDL receptor ligand-binding repeat homology <LDLC>

F;2605-2639/Domain: LDL receptor ligand-binding repeat homology <LDLD>

F;2652-2688/Domain: LDL receptor ligand-binding repeat homology <LDLE>

F;2696-2730/Domain: LDL receptor ligand-binding repeat homology <LDLF>

F;2734-2769/Domain: LDL receptor ligand-binding repeat homology <LDLG>

F;2774-2812/Domain: LDL receptor ligand-binding repeat homology <LDLH>

F;2818-2853/Domain: LDL receptor ligand-binding repeat homology <LDLI>

F;2858-2897/Domain: LDL receptor ligand-binding repeat homology <LDLJ>

F;2904-2939/Domain: LDL receptor ligand-binding repeat homology <LDLK>

F;2944-2980/Domain: EGF homology <EG11>

F;2986-3021/Domain: EGF homology <EG12>

F;3029-3068/Domain: LDL receptor WYTD-containing repeat homology <YW34>

F;3069-3113/Domain: LDL receptor WYTD-containing repeat homology <YW35>

F;3114-3156/Domain: LDL receptor WYTD-containing repeat homology <YW36>

F;3157-3200/Domain: LDL receptor WYTD-containing repeat homology <YW37>

F;3201-3241/Domain: LDL receptor WYTD-containing repeat homology <YW38>

F;3242-3284/Domain: LDL receptor WYTD-containing repeat homology <YW39>

F;3294-3330/Domain: EGF homology <EG13>

F;3334-3369/Domain: LDL receptor ligand-binding repeat homology <LDLM>

F;3374-3408/Domain: LDL receptor ligand-binding repeat homology <LDLN>

F;3413-3448/Domain: LDL receptor ligand-binding repeat homology <LDLO>

F;3453-3489/Domain: LDL receptor ligand-binding repeat homology <LDLP>

F;3494-3531/Domain: LDL receptor ligand-binding repeat homology <LDLQ>

F;3536-3570/Domain: LDL receptor ligand-binding repeat homology <LDLR>

F;3575-3609/Domain: LDL receptor ligand-binding repeat homology <LDLS>

F;3613-3647/Domain: LDL receptor ligand-binding repeat homology <LDLT>

F;3654-3690/Domain: LDL receptor ligand-binding repeat homology <LDLU>

F;3695-3731/Domain: LDL receptor ligand-binding repeat homology <LDLV>

F;3741-3776/Domain: LDL receptor ligand-binding repeat homology <LDLW>

F;3785-3822/Domain: EGF homology <EG14>

F;3828-3860/Domain: EGF homology <EG15>

F;3868-3911/Domain: LDL receptor WYTD-containing repeat homology <YW40>

A:Molecule type: mRNA

A:Residues: 1-28;4416-4453 <VAN2>

A:Cross-references: UNIPARC:UPI00001736D8; UNIPARC:UPI00001736D9; EMBL:X67469

C:Complex: The alpha-2-macroglobulin receptor complex consists of noncovalently-associated protein (see PIR:J0281).

C:Superfamily: alpha-2-macroglobulin receptor; EGF homology; LDL receptor ligand-binding; glycoprotein

C:Keywords: beta-hydroxyasparagine; beta-hydroxyaspartic acid; calcium binding; glycoprotein

F:1-19/Domain: signal sequence #status predicted <SIG>

F:20-3944/Domain: alpha-2-macroglobulin receptor #status predicted <MAT>

F:20-3944/Domain: alpha-2-macroglobulin receptor 515K chain #status predicted <515K>

F:28-65/Domain: LDL receptor ligand-binding repeat homology <LDL1>

F:73-109/Domain: LDL receptor ligand-binding repeat homology <LDL2>

F:116-149/Domain: EGF homology <EG1>

F:155-189/Domain: EGF homology <EG2>

F:199-240/Domain: LDL receptor WYTD-containing repeat homology <YW01>

F:241-282/Domain: LDL receptor WYTD-containing repeat homology <YW02>

F:293-335/Domain: LDL receptor WYTD-containing repeat homology <YW03>

F:336-379/Domain: LDL receptor WYTD-containing repeat homology <YW04>

F:380-421/Domain: LDL receptor WYTD-containing repeat homology <YW05>

F:422-469/Domain: LDL receptor WYTD-containing repeat homology <YW06>

F:479-520/Domain: EGF homology <EG3>

F:572-614/Domain: LDL receptor WYTD-containing repeat homology <YW07>

F:615-660/Domain: LDL receptor WYTD-containing repeat homology <YW08>

F:661-711/Domain: LDL receptor WYTD-containing repeat homology <YW09>

F:712-753/Domain: LDL receptor WYTD-containing repeat homology <YW10>

F:754-800/Domain: LDL receptor WYTD-containing repeat homology <YW11>

F:808-843/Domain: EGF homology <EG4>

F:855-891/Domain: LDL receptor ligand-binding repeat homology <LDL3>

F:896-932/Domain: LDL receptor ligand-binding repeat homology <LDL4>

F:937-972/Domain: LDL receptor ligand-binding repeat homology <LDL5>

F:977-1012/Domain: LDL receptor ligand-binding repeat homology <LDL6>

F:1016-1052/Domain: LDL receptor ligand-binding repeat homology <LDL7>

F:1063-1098/Domain: LDL receptor ligand-binding repeat homology <LDL8>

F:1105-1141/Domain: LDL receptor ligand-binding repeat homology <LDL9>

F:1146-1183/Domain: LDL receptor ligand-binding repeat homology <LDLA>

F:1186-1222/Domain: EGF homology <EG5>

F:1228-1262/Domain: EGF homology <EG6>

F:1270-1309/Domain: LDL receptor WYTD-containing repeat homology <YW12>

F:1310-1356/Domain: LDL receptor WYTD-containing repeat homology <YW13>

F:1357-1399/Domain: LDL receptor WYTD-containing repeat homology <YW14>

F:1400-1446/Domain: LDL receptor WYTD-containing repeat homology <YW15>

F:1447-1489/Domain: LDL receptor WYTD-containing repeat homology <YW16>

F:1490-1532/Domain: LDL receptor WYTD-containing repeat homology <YW17>

F:1541-1579/Domain: EGF homology <EG7>

F:1584-1627/Domain: LDL receptor WYTD-containing repeat homology <YW18>

F:1628-1670/Domain: LDL receptor WYTD-containing repeat homology <YW19>

F:1671-1714/Domain: LDL receptor WYTD-containing repeat homology <YW20>

F:1715-1754/Domain: LDL receptor WYTD-containing repeat homology <YW21>

F:1755-1797/Domain: LDL receptor WYTD-containing repeat homology <YW22>

F:1798-1847/Domain: LDL receptor WYTD-containing repeat homology <YW23>

F:1851-1887/Domain: EGF homology <EG8>

F:1935-1977/Domain: LDL receptor WYTD-containing repeat homology <YW24>

F:1978-2020/Domain: LDL receptor WYTD-containing repeat homology <YW25>

F:2021-2064/Domain: LDL receptor WYTD-containing repeat homology <YW26>

F:2065-2106/Domain: LDL receptor WYTD-containing repeat homology <YW27>

F:2107-2152/Domain: LDL receptor WYTD-containing repeat homology <YW28>

F:2160-2195/Domain: EGF homology <EG9>

F:2200-2242/Domain: LDL receptor WYTD-containing repeat homology <YW29>

F:2254-2295/Domain: LDL receptor WYTD-containing repeat homology <YW30>

F:2345-2389/Domain: LDL receptor WYTD-containing repeat homology <YW31>

F:2390-2430/Domain: LDL receptor WYTD-containing repeat homology <YW32>

F:2431-2474/Domain: LDL receptor WYTD-containing repeat homology <YW33>

F:2483-2518/Domain: EGF homology <EG10>

F:2525-2562/Domain: LDL receptor ligand-binding repeat homology <LDLB>

F:2567-2601/Domain: LDL receptor ligand-binding repeat homology <LDLC>

F:2606-2640/Domain: LDL receptor ligand-binding repeat homology <LDLD>

F:2653-2689/Domain: LDL receptor ligand-binding repeat homology <LDLE>

F:2697-2731/Domain: LDL receptor ligand-binding repeat homology <LDLF>

F:2735-2770/Domain: LDL receptor ligand-binding repeat homology <LDLG>

F:2775-2813/Domain: LDL receptor ligand-binding repeat homology <LDLH>

F:2819-2854/Domain: LDL receptor ligand-binding repeat homology <LDLI>

F:2859-2898/Domain: LDL receptor ligand-binding repeat homology <LDLJ>

F:2905-2940/Domain: LDL receptor ligand-binding repeat homology <LDLK>

F:2945-2981/Domain: EGF homology <EG11>
F:2987-3022/Domain: EGF homology <EG12>
F:3030-3069/Domain: LDL receptor WYTD-containing repeat homology <YW34>
F:3070-3114/Domain: LDL receptor WYTD-containing repeat homology <YW35>
F:3115-3157/Domain: LDL receptor WYTD-containing repeat homology <YW36>
F:3158-3201/Domain: LDL receptor WYTD-containing repeat homology <YW37>
F:3202-3242/Domain: LDL receptor WYTD-containing repeat homology <YW38>
F:3243-3285/Domain: LDL receptor WYTD-containing repeat homology <YW39>
F:3295-3331/Domain: EGF homology <EG13>
F:3335-3370/Domain: LDL receptor ligand-binding repeat homology <LDL1>
F:3375-3409/Domain: LDL receptor ligand-binding repeat homology <LDL2>
F:3414-3449/Domain: LDL receptor ligand-binding repeat homology <LDL3>
F:3454-3490/Domain: LDL receptor ligand-binding repeat homology <LDL4>
F:3495-3532/Domain: LDL receptor ligand-binding repeat homology <LDL5>
F:3537-3571/Domain: LDL receptor ligand-binding repeat homology <LDL6>
F:3576-3610/Domain: LDL receptor ligand-binding repeat homology <LDL7>
F:3614-3648/Domain: LDL receptor ligand-binding repeat homology <LDL8>
F:3655-3691/Domain: LDL receptor ligand-binding repeat homology <LDL9>
F:3696-3732/Domain: LDL receptor ligand-binding repeat homology <LDL10>
F:3742-3777/Domain: LDL receptor ligand-binding repeat homology <LDL11>
F:3786-3823/Domain: EGF homology <EG14>
F:3829-3861/Domain: EGF homology <EG15>
F:3869-3912/Domain: LDL receptor WYTD-containing repeat homology <YW40>
F:3913-3970/Domain: LDL receptor WYTD-containing repeat homology <YW41>
F:3945-4545/Domain: alpha-2-macroglobulin receptor 85K chain #status predicted <85K>
F:3945-4421/Domain: 85K chain extracellular #status predicted <EXT>
F:3971-4013/Domain: LDL receptor WYTD-containing repeat homology <YW42>
F:4014-4057/Domain: LDL receptor WYTD-containing repeat homology <YW43>
F:4058-4100/Domain: LDL receptor WYTD-containing repeat homology <YW44>
F:4101-4143/Domain: LDL receptor WYTD-containing repeat homology <YW45>
F:4152-4193/Domain: EGF homology <EG16>
F:4201-4232/Domain: EGF homology <EG17>
F:4237-4268/Domain: EGF homology <EG18>
F:4273-4304/Domain: EGF homology <EG19>
F:4309-4340/Domain: EGF homology <EG20>
F:4345-4375/Domain: EGF homology <EG21>
F:4378-4409/Domain: EGF homology <EG22>
F:4422-4445/Domain: transmembrane #status predicted <TM>
F:4446-4545/Domain: intracellular #status predicted <INT>
F:167,2993/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted
F:2959/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted
F:4076,4156,4279/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 6.1%; Score 131; DB 1; Length 4545;
Best Local Similarity 19.8%; Pred. No. 0.052;
Matches 78; Conservative 39; Mismatches 131; Indels 146; Gaps 21;

QY 62 GSCTSSLSRPLPLEESAMSADCLEAAEQLRNSSLIDCRCHRM-----KHQATCL 111
DB 2616 GSCIGNSSR-----CNQFVDCEDASDEM-NCSATDCSSVFRIGVKGVLFPQCERTSLCY 2668

QY 112 DIYVTHVPARSLGDYELDVSPYEDTVTSKPKWKNLSKLNMLKPDSDLCLKFAMLCITLHDK 171
DB 2669 APSWVDCGANDCGD-----YSDERDCPGVKPRCPPLNYFACPGRCIPMSWTCDKEDD 2721

QY 172 CDRLRKAYGE-----ACS-GIRQHLCLAQ-----LRSFPEKAESHAQG-- 211
DB 2722 CEN-----GEDETHCNKFCSEAQFEQONHRCISKQWLCDGSDDCGGGSEAA--HCEGKT 2774

QY 212 ----LLIICP-----CAPE-----DAGCGERR----RNTI----- 232
DB 2775 CGPSSFCPTGTHVCPERWLCDGDKDCTDGDAGESVTAGCLYNSTCDREPMQNRLCIPK 2834

QY 233 -----APSCALPSVTPN-----CLDRSF-CRADPLCRSRIMDFQT 267
DB 2835 HFVCDHRRDCADGSDSEPEYTCGNEFRFCANGRCSSRQWECDEGNDCHDHSDEAPK 2894

QY 268 HCHPMDILGTCAEQSRCLRAYLGLTGATMPNFIKVVNTVALSCTCRSGNLDQEC-- 325
DB 2895 NPH-----CTSPFHKC-----NASSQFLCSSGRVCVABALLCNG-----QDDCGD 2933

QY 326 EQLERSFSQNPCLVEAIAAKMRFHQLFSDQWAD 359

Db 2934 GSDRGCHVNECLSRKLSG-----CSQDCED 2959

RESULT 4
E89753
protein F11C7.4 [imported] - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: E89753
R:Anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biology
A:Reference number: A75000; MUID:99069613; PMID:9851916
A:Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_elegans/
A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; an
A:Accession: E89753
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1722 <STO>
A:Cross-references: UNIPROT:Q19350; UNIPARC:UPI0000074975; GB:chr_X; PIDN:AAC69012.1; P
C:Genetics:
A:Gene: F11C7.4
A:Map position: X

Query Match 5.8%; Score 124; DB 2; Length 1722;
Best Local Similarity 19.9%; Pred. No. 0.071;
Matches 75; Conservative 53; Mismatches 156; Indels 92; Gaps 21;

QY 34 ENRFVNSTQ---ARKKC---BANPACAAAYOHLGS-CTSSLSRPLPLEESAMSADCLEA 86
DB 1327 EQRDVNECNHYDCNRGHCVMTVSGPACQCEMGYTGRCFKLJN-----QCSNNTCSSRGA 1381

QY 87 AQLRNSSLIDC-----RCHRMKHQATCLDIYVTHVPARSLGDYELDVSPYEDTVTS 139
DB 1382 CSPVWNNTVCNDDNNWRGAHQHMD---TCLDF-----PCWNDG----- 1418

QY 140 KPWKNLSKLNMLKPDSDLCLKFAM--LCTLHDKDRLRKAYGEACSGIRCORHLCLAQ 197
DB 1419 -----VCTNDENTFSCQKQFFMGTRCEIISGSLCAQCVHGE-CIQLSPETHTCSNI 1471

QY 198 RSFFKAESHAQGLLLCPACPEDAGCGRRRNTTAPSCALPSVTPNC---LD--LRSPC 252
DB 1472 -GYEGDCAKCKIDYCKAGPCL-NGANC-ENKLTGYKCTCAVGFEGADCEINIDCALEFC 1528

QY 253 RADPLCRSLMDPQTHCHPMDILG--TCATEQSRCLRAYLGLTGATMPNFIK--VNTTV 309
DB 1529 KNGAKCRDKINDYECVCDGTGFGEGNCTTDINEC-----ANPNINCINGECTNTLG 1578

QY 310 ALSCTCRSGNLDQECQELERSFSQNPCLVEAIAAKMRFHQLFSDQWADTSFVVQQQN 369
DB 1579 NYKCACR-NGFIGPRCS-----VRNPCTAQIASNNI-----SSVTCVHGKC 1618

QY 370 SNPALRLQPLRLILSF 385
DB 1619 VNPVQVQIEKNREVAKY 1634

RESULT 5
T09059
notch4 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C:Accession: T09059
R:Rowen, L.; Mahairas, G.; Qin, S.; Ahearn, M.E.; Dankers, C.; Loretz, C.; S.
submitted to the EMBL Data Library, October 1997
A:Description: Sequence of the mouse major histocompatibility locus class III region.
A:Reference number: Z16543
A:Accession: T09059
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1964 <ROW>
A:Cross-references: UNIPROT:P31695; UNIPARC:UPI000016C7F1; EMBL:AF030001; NID:g2564945;
C:Genetics:

A;Gene: notch4
A;Map position: 17
A;Introns: 22/1; 49/2; 148/1; 264/1; 305/1; 384/1; 436/1; 501/1; 539/1; 577/1; 618/1; 671/3; 1729/1; 1761/3
C;Superfamily: notch protein; ankyrin repeat homology; EGF homology
C;Keywords: receptor; signal transduction
F;514-545/Domain: EGF homology <EGF>

Query Match 5.8%; Score 123; DB 2; Length 1964;
Best Local Similarity 22.6%; Pred. No. 0.099;
Matches 81; Conservative 33; Mismatches 156; Indels 88; Gaps 19;

QY 40 SCTQARKKCRANP-----ACKAAVQHIG-SCSSLSRPLPLEESAMSDCL 84
Db TCSEEVATCHSGPLNGSGSIRPEGYSCTCLPSHTGRHCQTAV-----DHCVSASCL 774

QY 85 EA-----AEQLRNSLLDCECHRMKHOATCLDIYVTHPARS 122
Db 775 NGGTCVNKPTFFCLCATGFGQLHCEBKTNPSCADSPC-----RNKATCQD---TPRGARC 827

QY 123 L---GDYELDVSPYEDVTTSKPMKMLSKLMLKPDSDCLK--FAMLCCTLHDKCDRLRK 177
Db 828 LCSFGYTGSSCOTLIDLCAKPCPHPTARCLQSGSPFCCLQGTGALCDFPLSCQKAA 887

QY 178 AYEACSGIRQOR-HLCLAQLRFFFEKAAESHAQGLL-----LCPCAPEDAGCGERRNTI 232
Db 888 SQGIEISGL-CQNGGLCIDTSSVFCRPPGF-QGKLQDNVNPCEPNCHHG-----STC 941

QY 233 AP-----SCALPSVTPNCLDLRSFCRADP-----LCRSRLMDFQTHCHPMILGTCA 280
Db 942 VPQSGYVQCAPFEGYQNCQSKVLDAQSQPCFCHNHGTCTSRPGGFHCACPPGFVGLRCEG 1001

QY 281 EQSKRLRAYLGLIGTATPMFISKVVNTVALSTCRGSGNLOCEOLERSFSQNP-PC 337
Db 1002 DVDECLDRPCHPSGTAACHSLAN-----AFYCCQL-PGHTGQRCZ-VEMDLQSQGPC 1051

RESULT 6
A46019
notch-1 protein - mouse
N;Alternate names: notch protein
C;Species: Mus musculus (house mouse)
C;Date: 22-Sep-1993 #sequence revision 18-Nov-1994 #text change 05-Oct-2004
C;Accession: A46019; S25144; C49175; B46438; PH1569; S32109
R;Del Amo, F.P.; Gendron-Maguire, M.; Swiatek, P.J.; Jenkins, N.A.; Copeland, N.G.; Grid
Genomics 15, 259-264, 1993
A;Title: Cloning, analysis, and chromosomal localization of Notch-1, a mouse homolog of
A;Reference number: A46019; MUID:93194170; PMID:8449489
A;Accession: A46019
A;Status: not compared with conceptual translation
A;Molecule type: nucleic acid
A;Residues: 1-2531
A;Cross-references: UNIPROT:Q01705; UNIPARC:UPI000002922B; GB:S477228; NID:928
A;Note: sequence extracted from NCBI backbone (NCBI:P127318)
R;Franco del Amo, F.; Smith, D.E.; Swiatek, P.J.; Gendron-Maguire, M.; Greenspan, R.J.;
submitted to the EMBL Data Library, April 1992
A;Description: Expression pattern of Notch, a mouse homolog of Drosophila Notch, suggest
A;Reference number: S25144
A;Accession: S25144
A;Molecule type: mRNA
A;Residues: 1551-2108, 'Q', 2110-2114, 'ALP', 2118-2170 <PRA>
A;Cross-references: UNIPARC:UPI0000177461; EMBL:Z11886
R;Lardelli, M.; Lendahl, U.
Exp. Cell Res. 204, 364-372, 1993
A;Title: Notch A and Notch B--two mouse Notch homologues coexpressed in a wide variety of
A;Reference number: A49175; MUID:93178563; PMID:8440332
A;Accession: C49175
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1161-1547 <LAP>
A;Cross-references: UNIPARC:UPI0000177462; EMBL:X68278; NID:G287987; PIDN:CAA48339.1; PI
A;Experimental source: embryo
A;Note: sequence extracted from NCBI backbone (NCBI:P126159)

R;Kopan, R.; Weintraub, H.
J. Cell Biol. 121, 631-641, 1993
A;Title: Mouse notch: expression in hair follicles correlates with cell fate determinat
A;Reference number: A46438; MUID:93252998; PMID:8486742
A;Accession: B46438
A;Status: preliminary
A;Molecule type: nucleic acid
A;Residues: 1865-1932, 'RR', 1935-1937, 'L', 1938-1967, 'I', 1969-2044, 'IB', 2047-2052, 'S', 205
A;Cross-references: UNIPARC:UPI0000177463
A;Experimental source: embryo
A;Note: sequence extracted from NCBI backbone (NCBI:P131246, NCBI:P131247)
C;Comment: This protein has many EGF repeats and lin-12[1172]/Notch repeats.
C;Genetics:
A;Gene: notch-1
A;Map position: 2
A;Note: proximal region of chromosome 2
C;Superfamily: notch protein; ankyrin repeat homology; EGF homology
F;106-138/Domain: EGF homology <EGF1>
F;144-175/Domain: EGF homology <EGF1>
F;222-254/Domain: EGF homology <EGF2>
F;261-292/Domain: EGF homology <EGF2>
F;339-370/Domain: EGF homology <EGF3>
F;416-449/Domain: EGF homology <EGF3>
F;456-487/Domain: EGF homology <EGF4>
F;494-525/Domain: EGF homology <EGF5>
F;532-563/Domain: EGF homology <EGF6>
F;607-638/Domain: EGF homology <EGF7>
F;682-713/Domain: EGF homology <EGF8>
F;757-788/Domain: EGF homology <EGF9>
F;795-826/Domain: EGF homology <EGF10>
F;873-904/Domain: EGF homology <EGF11>
F;911-942/Domain: EGF homology <EGF12>
F;949-980/Domain: EGF homology <EGF13>
F;987-1018/Domain: EGF homology <EGF14>
F;1025-1056/Domain: EGF homology <EGF15>
F;1063-1094/Domain: EGF homology <EGF16>
F;1149-1180/Domain: EGF homology <EGF17>
F;1187-1218/Domain: EGF homology <EGF18>
F;1233-1264/Domain: EGF homology <EGF19>
F;1352-1383/Domain: EGF homology <EGF19>
F;1391-1425/Domain: EGF homology <EGF>
F;1917-1948/Domain: ankyrin repeat homology <AN1>
F;1949-1981/Domain: ankyrin repeat homology <AN2>
F;1983-2015/Domain: ankyrin repeat homology <AN3>
F;2016-2048/Domain: ankyrin repeat homology <AN4>
F;2049-2081/Domain: ankyrin repeat homology <AN5>

Query Match 5.7%; Score 120.5; DB 2; Length 2531;
Best Local Similarity 19.7%; Pred. No. 0.2;
Matches 84; Conservative 45; Mismatches 130; Indels 167; Gaps 26;

QY 39 NSTQARKKEANPACAAVQHIGSCSSLSRPL-----PLEESAMSD-CLEAAEQLRNS 94
Db 379 NPCNEG-SNCDTNP-----VNGKRICTCPGTYGSPACSDVDECDLGANRCEHAGKCLNTLG 434

QY 95 LIDCRC-----HRRMKHOATCLDIYVTHPARSLGDVLDVSP-VE-- 134
Db 435 SFECCQLQGTGPGCEIDVNECISNFCQNDATCLD-----QIGFQCICMPGYEGV 495

QY 135 -----DVTSTKPMKMN-----LSKL-----NMLKPDSDCLK----- 161
Db 486 YCEINTDECASSPLNGHGMCKIHEFCQCQPKGFNGHLCQYDVDECASTPCKNGAKCLD 545

QY 162 -----FAMLCI-----LH-----DKDRLKAYCEACSGIR-----CQ-----RHLCLAQLR 198
Db 546 GPNYTCVCTGEGYTGTHCEVDIDECDDPCHYGSCDKGVATFTCLCQPGYTGHCFTNIN 605

QY 199 SPFEKAAESHAQGLLCLPCAPEDAGCGERRNTIAPSICALPSVTPNCLDLRSFCRADP-- 256
Db 606 -----ECHSQ-----PC--RHGGTCQDRDINSYLCCLKGLTGTPNCEINLDCASNPCD 651

QY 257 --LCRSRLMDFQTHCHP-----MDIL-----GTC-----ATBQSRLRAYLGL 292

Db	652	SGTCLDKIDGYEACAEFGYGTGSMCNVNIDECAGSPCHNGTCTEDGIAGFTCKCPGY----	708
Qy	293	IGTAMTPNFISKVNTTVALSC---TCRGSNG-----LQDECEQLRSF	332
Db	709	----HDP TCLSEVNECNSNPCIHGACRDGLNGYKDCAPGWSGTNCDINNNECE-----	758
Qy	333	SQNPKL	338
Db	759	-SNPCV	763
RESULT 7			
A40043			
notch protein homolog TAN-1 precursor - human			
C:Species: Homo sapiens (man)			
C>Date: 21-Apr-1992 #sequence_revision 21-Apr-1992 #text_change 05-Oct-2004			
C:Accession: A40043			
R:Ellisen, L.W.; Bird, J.; West, D.C.; Soreng, A.L.; Reynolds, T.C.; Smith, S.D.; Sklar, Cell 66, 649-661, 1991			
A:Title: TAN-1, the human homolog of the Drosophila Notch gene, is broken by chromosomal			
A:Reference number: A40043; MUID:91347367; PMID:1831692			
A:Accession: A40043			
A>Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra			
A:Molecule type: mRNA			
A:Residues: 1-2555 <ELI>			
A:Cross-references: UNIPARC:UPI000177455; GB:M73980			
C:Superfamily: notch protein; ankyrin repeat homology; EGF homology			
F:261-292/Domain: EGF homology <EGX1>			
F:494-525/Domain: EGF homology <EGFL>			
F:987-1018/Domain: EGF homology <EGK2>			
F:1149-1180/Domain: EGF homology <EGF>			
F:1187-1218/Domain: EGF homology <EGF3>			
F:1233-1264/Domain: EGF homology <EGX3>			
F:1927-1959/Domain: ankyrin repeat homology <AN1>			
F:1960-1992/Domain: ankyrin repeat homology <AN2>			
F:1994-2026/Domain: ankyrin repeat homology <AN3>			
F:2021-2059/Domain: ankyrin repeat homology <AN4>			
F:2060-2092/Domain: ankyrin repeat homology <AN5>			
Query Match 5.5%; Score 118; DB 2; Length 2555;			
Best Local Similarity 20.4%; Pred. No. 0.33;			
Matches 85; Conservative 46; Mismatches 136; Indels 150; Gaps 26;			
Qy	39	NSTQARKKEANPACKAAYQHLGCTSSLSRPL-----PLEESAMSD-CLEAAEQLRNSS	94
Db	379	NPCNEG-SNCDTNPVNGKA---ICTCPSGYTGPAQSQDVDECSLGNPCHEHAGKINTLG	434
Qy	95	LIDCRC-----HRRMKHOATCLDIYTWVHPARSLGVDYELVSP-YE--	134
Db	435	SPECQLQGYTGPRCIDVNECVSNPCQNDATCLD-----QIGEFQCMFPGYEGY	485
Qy	135	-----DVTSTKPKWKN-----LSKLN-----MLKPSDLCLK-----	161
Db	486	HCEVNTDECASSFLANGRCGLDKINEFQCEPCTGFTGHLQDVDECASTCKNGAKCLDG	545
Qy	162	----FAMLC-----LH-----DKCDRLRKAYGACSGIRQHRHCLQAQLRSFEKAAESH	208
Db	546	PNITYTCVCTEGYTGTHCEVDIDCEDPDPCHYGCKDGVATFTCLCRP-----GYTGHHCETN	602
Qy	209	AQGLLLCPCA-----PEDAGGERRRNTIAPSCAL-----PSVTPNCLD-LRSE-	251
Db	603	INESSQPCNLRGTQCDPDNAYLCFLCKGTGTGNCINLDDCASSPCDSGTCLDKIDGYE	662
Qy	252	CRADP-----LCRSRLMDFOTH-CHPMDILGTCATE-----QSRCLRAYLGLIGTAMTPNF	301
Db	663	CACEPGYGTGSMCNINDECAGNPCNG---GTCTEDGINGFTCRCPGY-----HDP TC	712
Qy	302	ISKVNTTVALSC---TCRGSNG-----LQDECEQLRSFSQNPKL	338
Db	713	LSEVNECNSNPCVHAGACRDSLNGYKDCDPPGWSGTNCDINNNECE-----SNPCV	762

RESULT 8			
S19694			
tenascin precursor - pig			
N:Alternate names: contactin; hexabrachion			
C:Species: Sus scrofa domestica (domestic pig)			
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004			
C:Accession: S19694			
R:Niehi, T.; Weinstein, J.; Gillespie, W.M.; Paulson, J.C.			
Eur. J. Biochem. 202, 643-648, 1991			
A:Title: Complete primary structure of porcine tenascin. Detection of tenascin transcrip			
A:Reference number: S19694; MUID:92104189; PMID:1722152			
A:Accession: S19694			
A:Molecule type: mRNA			
A:Residues: 1-1746 <NIS>			
A:Cross-references: UNIPROT:Q29116; UNIPARC:UPI000136BBB; EMBL:X61599; NID:g2124; PIDN			
C:Superfamily: tenascin; EGF homology; fibronogen beta/gamma homology; fibronectin type			
C:Keywords: alternative splicing; calcium binding; cell adhesion; duplication; extracel			
F:1-22/Domain: signal sequence #status predicted <SIG>			
F:23-1746/Product: tenascin #status predicted <MAT>			
F:346-372/Domain: EGF homology <EGF>			
F:377-403/Domain: EGF homology <EGF2>			
F:622-703/Domain: fibronectin type III repeat homology <FN3A>			
F:711-793/Domain: fibronectin type III repeat homology <FN3B>			
F:802-884/Domain: fibronectin type III repeat homology <FN3C>			
F:892-976/Domain: fibronectin type III repeat homology <FN3D>			
F:984-1064/Domain: fibronectin type III repeat homology <FN3E>			
F:1073-1155/Domain: fibronectin type III repeat homology <FN3F>			
F:1164-1246/Domain: fibronectin type III repeat homology <FN3G>			
F:1254-1335/Domain: fibronectin type III repeat homology <FN3H>			
F:1343-1423/Domain: fibronectin type III repeat homology <FN3I>			
F:1431-1511/Domain: fibronectin type III repeat homology <FN3J>			
F:1526-1734/Domain: fibronogen beta/gamma homology <FBG>			
F:38,166,184,327,788,1034,1079,1121,1354/Binding site: carbohydrate (asn) (covalent) #s			
Query Match 5.5%; Score 117; DB 1; Length 1746;			
Best Local Similarity 21.5%; Pred. No. 0.27;			
Matches 90; Conservative 33; Mismatches 150; Indels 146; Gaps 22;			
Qy	43	QARKKEANPACKAAYQHLGCTSSLSRPLPLEESAMSDCLEAAEQLRNSSLIDCRCHR	102
Db	351	RGRGRCEE-----GQCV-----CDEGFAGADCSE-----RCPS	379
Qy	103	RMKHOATCLDIYTWVHPARSLGVDYELVSPYEDTVTSPKQNLKLNMLKPSDLCL--L	160
Db	380	DCHNRGCLD-----GRCECD-DGFE-----GEDCGEL	406
Qy	161	KFAMLC TLHDK-----CDRLRKAYGACSGIRQ-----RHLCLAQLRSFEKAAESH	208
Db	407	RCFGGSGHGRVCVNGQCVQCDGRT--GEDCSQLRCPNDCHGRGCV-QGRCEHGFQGY	463
Qy	209	AQGLLLCP-----CAPEDAGGERRRNTIAPS-----CALPSV	241
Db	464	DCEMSCPHDC HQHGRGCVNGMCVDDGYTGDCRELRCPGDCSQRGRCVDCRGVCEHGA	523
Qy	242	TPNCLDLRSFCRADPLCRSRLMDFQTHC-----PMDI--LGTCAEQSRCL	286
Db	524	GPDCADLA--CFSDCHGRGRCVNGCVCHEGFTGDKGQRRCPGDCHGGRVCVGGCVCH	581
Qy	287	RAYLGL-IGTAMTPNFISKVNTTVALSCTCRSGNMLQDECEQLRSFSQNPKLVEIAAA-	344
Db	582	EGFTGLDCQQRSCPNDCSNWQCVSGRCIC-NEGYSGEDCSQVS---PPKDLIVTVEE	637
Qy	345	-----KMRFHROLF-----SQWADSTFVQQNSNPALRQPLRP--ILSFSIL	388
Db	638	TYNLAWDNEMRWTEYLIVYTPHEDGLEMQFRVPGDQTSTTIRELEPGVEYFIRVAIL	696

RESULT 9			
A53102			
alpha-2-macroglobulin receptor precursor - chicken			
N:Alternate names: CD91; LDL receptor-related protein 1; low density lipoprotein recept			
C:Species: Gallus gallus (chicken)			
C>Date: 04-Sep-1998 #sequence_revision 04-Sep-1998 #text_change 09-Jul-2004			

C;Accession: A53102

R;Nimpt, J.; Stifani, S.; Bilous, P.T.; Schneider, W.J.

J. Biol. Chem. 269, 212-219, 1994

A;Title: The somatic cell-specific low density lipoprotein receptor-related protein of b

A;Reference number: A53102; MUID:94103212; PMID:7506255

A;Accession: A53102

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-4543 <NIM>

A;Cross-references: UNIPROT:P98157; UNIPARC:UPI000013C4B3; GB:X74904; NID:G438006; PIDN

C;Complex: The alpha-2-macroglobulin receptor complex consists of noncovalently-associated

d protein.

C;Superfamily: alpha-2-macroglobulin receptor; EGF homology; LDL receptor ligand-binding

C;Keywords: beta-hydroxyasparagine; beta-hydroxyaspartic acid; calcium binding; glycopro

F;1-17/Domain: signal sequence #status predicted <SIG>

F;18-3942/Domain: alpha-2-macroglobulin receptor 515K chain #status predicted <515K>

F;3239-3281/Domain: LDL receptor WYTD-containing repeat homology <LDL1>

F;3291-3327/Domain: EGF homology <EG13>

F;3331-3366/Domain: LDL receptor ligand-binding repeat homology <LDL2>

F;3371-3405/Domain: LDL receptor WYTD-containing repeat homology <EG2>

F;3410-3445/Domain: LDL receptor WYTD-containing repeat homology <YW01>

F;3450-3486/Domain: LDL receptor ligand-binding repeat homology <YW02>

F;3491-3528/Domain: LDL receptor ligand-binding repeat homology <YW03>

F;3533-3567/Domain: LDL receptor ligand-binding repeat homology <YW04>

F;3572-3606/Domain: LDL receptor ligand-binding repeat homology <YW05>

F;3610-3644/Domain: LDL receptor ligand-binding repeat homology <YW06>

F;3651-3687/Domain: LDL receptor WYTD-containing repeat homology <YW07>

F;3692-3728/Domain: LDL receptor WYTD-containing repeat homology <YW08>

F;3738-3774/Domain: LDL receptor WYTD-containing repeat homology <YW09>

F;3783-3820/Domain: EGF homology <EG3>

F;3826-3858/Domain: LDL receptor WYTD-containing repeat homology <YW10>

F;3866-3909/Domain: LDL receptor WYTD-containing repeat homology <YW11>

F;3910-3968/Domain: LDL receptor WYTD-containing repeat homology <LDL3>

F;3943-4420/Domain: 85K chain extracellular #status predicted <EXT>

F;3969-4011/Domain: LDL receptor WYTD-containing repeat homology <LDL4>

F;4012-4055/Domain: LDL receptor WYTD-containing repeat homology <LDL5>

F;4056-4098/Domain: LDL receptor WYTD-containing repeat homology <LDL6>

F;4099-4141/Domain: LDL receptor WYTD-containing repeat homology <LDL7>

F;4150-4181/Domain: EGF homology <EG16>

F;4199-4230/Domain: EGF homology <EG17>

F;4235-4266/Domain: EGF homology <EG18>

F;4271-4302/Domain: EGF homology <EG19>

F;4307-4338/Domain: EGF homology <EG20>

F;4343-4373/Domain: EGF homology <EG21>

F;4376-4408/Domain: EGF homology <EG22>

F;4421-4443/Domain: transmembrane #status predicted <TM>

F;4444-4543/Domain: intracellular #status predicted <INT>

F;116,138,187,276,359,448,731,926,1152,1153,1193,1216,1305,1509,1556,1573,1614,1633

3485,3659,3786,3837,3952,4074,4124,4178,4278/Binding site: carbohydrate (Asn) (covalent

F;168,2995/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted

F;2955/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted

Query Match 5.5%; Score 117; DB 1; Length 4543;

Best Local Similarity 20.3%; Pred. No. 0.72;

Matches 65; Conservative 33; Mismatches 134; Indels 88; Gaps 16;

QY 29 NSLATENR-----VNSCTQARKKCANPACKAAYOHL-----GSCSTSLRPLPLESAMSA 81

Db 2569 NGRCVASRWCNGVDDGNSDEVFNKTSCTAETFCRCDGSCIGNSSR-----CNQFI 2622

QY 82 DCLAAARLNSSLIDCRCH-----RMKHOATCLDIYTWVHPARSIGDYELDVS 131

Db 2623 DCDASDEM-NCTATDCSSYFKLVKGKTTFFQKCENTSLCYAPSWCDGDCD----- 2675

QY 132 PYEDVTTSKPMONTSLNMLKPDSDLCLKFAMLTCLDKCDRLKAYGE---ACS--- 184

Db 2676 -YSDERNCPGGRKPKCPANYFACPGRCIPMTWTCKEDDCEN-----GEDSTHCERQD 2729

QY 185 -----GTRCQRHLCLAOLRSFFKAAE-----SHAQGLLCP-----CAP 219

Db 2730 KFCYVQPECNHRICSLK---WVCGADDCGSDSDSCRITTCSTGSGFCQGVVCP 2787

QY 220 E-----DAGCGERRNTIAPSCALPVPNCLRLSFCRADPLC---RSRLMDFQTHC--- 269

A;Cross-references: UNIPARC:UPI0000173D1F
 A;Note: the authors translated the codon ATC for residue 49 as Thr, ATT for residue 2044
 R;Tautz, D.
 Nucleic Acids Res. 17, 6463-6471, 1989
 A;Title: Hypervariability of simple sequences as a general source for polymorphic DNA markers
 A;Reference number: S09358; MUID:89385974; PMID:2780284
 A;Accession: S09358
 A;Molecule type: DNA
 A;Residues: 2505-2551, 'OQQO', 2552-2576, 'E', 2578-2604 <TAU>
 A;Cross-references: UNIPARC:UPI0000173D20
 R;Wharton, K.A.; Yedvobnick, B.; Finnerty, V.G.; Artavanis-Tsakonas, S.
 Cell 40, 55-62, 1985
 A;Title: opa: a novel family of transcribed repeats shared by the Notch locus and other
 A;Reference number: A05267; MUID:8509329; PMID:2981631
 A;Accession: A05267
 A;Molecule type: DNA
 A;Residues: 2504-2576, 'E', 2578-2611 <WHA2>
 A;Cross-references: UNIPARC:UPI0000173D21
 C;Genetics:
 A;Gene: notch; opa
 A;Cross-references: FlyBase:FBgn0004647
 A;Map position: 8.96-9.36
 A;Introns: 53/3; 84/3; 171/3; 240/3; 283/3; 2333/3; 2436/3; 2588/3
 C;Superfamily: notch protein; ankyrin repeat homology; EGF homology
 C;Keywords: differentiation; tandem repeat; transmembrane protein
 F;27-43/Domain: transmembrane #status predicted <TMW1>
 F;297-328/Domain: EGF homology <EGX1>
 F;530-561/Domain: EGF homology <EGP1>
 F;568-599/Domain: EGF homology <EGP>
 F;988-1019/Domain: EGF homology <EGX2>
 F;1064-1095/Domain: EGF homology <EGF3>
 F;1187-1218/Domain: EGF homology <EGX3>
 F;1746-1762/Domain: transmembrane #status predicted <TMW2>
 F;1950-1982/Domain: ankyrin repeat homology <AN1>
 F;1983-2015/Domain: ankyrin repeat homology <AN2>
 F;1988-2004/Domain: transmembrane #status predicted <TMW3>
 F;2017-2049/Domain: ankyrin repeat homology <AN3>
 F;2050-2082/Domain: ankyrin repeat homology <AN4>
 F;2083-2115/Domain: ankyrin repeat homology <AN5>
 F;2538-2568/Region: glutamine-rich
 F;2538-2568/Domain: neurogenic repetitive element #status predicted <OPA>

Query Match 5.3%; Score 112.5; DB 1; Length 2703;
 Best Local Similarity 21.6%; Pred. No. 0.98;
 Matches 76; Conservative 34; Mismatches 127; Indels 115; Gaps 20;

QY 40 SCTQARKKCEANPACKAAYQHLGS-----CTSSLRPLPLESAMSADCLAEAEQLRNS 93
 Db 1056 NCQYKLNKCDSPNCLNGATCHEQNNYETCHCPSGT-----GKQCEYVDWCGQS 1105
 QY 94 SLIDCRCHRRMCHQATC-LDIYTVHPARSLGDYELDVSPYEDTVTSKPKMNLKLNML 152
 Db 1106 PCENGATCSQMKQFSCSAGWT----- 1129
 QY 153 KPDSDLCLFAMLCITLHDKCDR-----LR-----KAYGEA-----CS-----GIRCORHL 192
 Db 1130 ---GKLCVDTISC--QDAADRKGLSLRQLCNGNTCKDYGNSHVCYCSQGVAGSYCQKEI 1184
 QY 193 --CLAQ-----LRSPFEKAESHAQG-----LLLCFCAP---EDAG-CGERRNTI 232
 Db 1185 DECSQPCQNGTGRDLIGAYECQCRQCGQNGELNIDPCAPNCPNGGTCHDRVNNF- 1243
 QY 233 APSCALPSVTPNCL-----DLR-SFCRADPLCHRSRLMDFTQCHPMDILGTCAEQSRC 285
 Db 1244 --SCSCPPTGWTGICEINKDDCKGACHNNGSCIDRVGGFCVQCQPFVGARCEGDINEC 1301
 QY 286 LRAYLGLIGTAMPNFISKVTNTVALSCTCRSGNLQDECEQLERSFSQNPIC 337
 Db 1302 LSNPCSNAGTL---DCVQLVNN---YHCNCR-PGHMGRHCEHKVDYFCAQSPC 1346

RESULT 13
 S62935

hypothetical protein YN1023c - yeast (Saccharomyces cerevisiae)
 N;Alternate names: hypothetical protein N2812
 C;Species: Saccharomyces cerevisiae
 C;Date: 27-Apr-1996 #sequence_revision 03-May-1996 #text_change 09-Jul-2004
 C;Accession: S62935; S62945
 R;Andre, B.; Iraqi Housaini, I.; Urrestarazu, L.A.; Visser, S.
 submitted to the Protein Sequence Database, April 1996
 A;Reference number: S62920
 A;Accession: S62935
 A;Molecule type: DNA
 A;Residues: 1-965 <AND>
 A;Cross-references: UNIPROT:P53971; UNIPARC:UPI0000053082; EMBL:Z71299; NID:gl301854; P;
 A;Experimental source: strain S288C
 R;Duesterhoeft, A.; Floeth, M.; Fritzt, C.; Heuss-Neitzel, D.; Hilbert, H.; Moestl, D.
 submitted to the Protein Sequence Database, April 1996
 A;Reference number: S62944
 A;Accession: S62945
 A;Molecule type: DNA
 A;Residues: 1-965 <DUE>
 A;Cross-references: UNIPARC:UPI0000053082; EMBL:Z71299; NID:gl301854; PID:e239870; PID;
 A;Experimental source: strain S288C
 C;Genetics:
 A;Gene: SGD:FAP1
 A;Cross-references: SGD:S0004968
 A;Map position: 14L

Query Match 5.2%; Score 110; DB 2; Length 965;
 Best Local Similarity 22.1%; Pred. No. 0.54; Mismatches 28; Indels 144; Gaps 22;
 Matches 77; Conservative 28; Mismatches 100; Indels 144; Gaps 22;

QY 42 TQARKKC-EANPACKAAYQHLGSCTSSL-----SRPLPLESAMSADCLAEAEQ 89
 Db 339 TKPRKHCDDPIPTCDS-----RCGKPLKCGKHSPTCHDKACMEPLQIDSVKCAEQ 392
 QY 90 -----LRNSSLIDCRCHRRMCHQATCLDIYTVHPARSLGDYELDVSPY 133
 Db 393 STFSVPCGFGQPRCNKIKESLMSRRHR-----CTDRCSSGRP----- 431
 QY 134 EDTVTSKPKMNLKLNMLKPD-----DLCLK-----FAMLCITLHDKCDRLRKAYGEACSG 185
 Db 432 ----SARRKKNLFRTQDLDLSLVEAKHICLPCNLTLSGGIH-KQR-----KCHP 479
 QY 186 IRCORHLCLAQRSFFEKAAESHAQGLLCP-----APDAGCGERRNTIAPSALPSV 241
 Db 480 GKCPP-CL-----ESDND-LVCPGCVTVVPAPVRCG-----TKLPTCNHPCI 520
 QY 242 TPNCLDLRSCFADPLCRSLRMDFTQCHPMDILGTCAEQSRCRLRAYLGLIGTAMP-- 299
 Db 521 -----KVVRGEGTCHKMPHT--CHSLDVSCPECTE-----TVFKPK 557
 QY 300 -NFISKVNTT---VALSC-----TCRSGNLQDECEQ 327
 Db 558 CGKTKRTVCFQTDVSCGKIGKGIPLSYCHTQKTCPLPNCQKVKCK 606

RESULT 14
 T18355

hypothetical protein P3 - Mycoplasma hyorhinis

C;Species: Mycoplasma hyorhinis
 C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C;Accession: T18355
 R;Deng, G.; McIntosh, M.A.
 J. Bacteriol. 176, 5929-5937, 1994
 A;Title: An amplifiable DNA region from the Mycoplasma hyorhinis genome.
 A;Reference number: Z18888; MUID:95014025; PMID:7928953
 A;Accession: T18355
 A;Status: preliminary; translated from GB/EMBL/DDB
 A;Molecule type: DNA
 A;Residues: 1-1187 <DEN>
 A;Cross-references: UNIPROT:Q49549; UNIPARC:UPI00000B9898; EMBL:L11447; NID:gl50156; P;
 C;Genetics:
 A;Genetic code: SGCS

Query Match 5.2%; Score 110; DB 2; Length 1187;
Best Local Similarity 18.8%; Pred. No. 0.67; Mismatches 116; Indels 126; Gaps 20;
Matches 65; Conservative 38; Mismatches 116; Indels 126; Gaps 20;

QY 41 CTQARRKCEANPACAAAYQHLSGCTSS---LSRPL-----PLEESAMADCL 84
DB 221 CANSKNVCDLCECN-----GQNEQIIVKEPVQEEPEEQATPEQPIELTDLEDDHF 274

QY 85 EAAEQRLNSLIDCRCHRRMKHQAATC-----LDIYVTHPARSLGDYELDVSPYEDT 136
DB 275 ETV-HLEEEVCLAC-----QHVATCDICKNLSHSEILYRLKNGQVNNLLETELETELH 327

QY 137 VTSKPKMNLKLNMLKPDSDCLKPFAMLCCL---HDKCDRLRKAYGEACSGIRCORHLC 193
DB 328 YADSP-----VOEGKEPC-----GCSLKETEECD-----CEACKQCEBENS 366

QY 194 LAQLRSFFEKABASHQAQLLCLPCAPEDAGCGRRRRNTIAPSCALPSVT-----PNCL 246
DB 367 CSELTGCGEAT-----CSCAQEHGCGQE-----SCACPNTTCACTEEHCECT 410

QY 247 DLRSFCRADPL-CRSRLMD-FQTHCHPMDILGTCAEQSRCLRAYLGLIGTAMTPNFIK 304
DB 411 ESTCGCENEPCEEEACDCSEHCE-----CVDETOACL-----D 446

QY 305 VNT---TVALSC-----TCRGSNQLQDECEQLERSFSQNPCLVSE 340
DB 447 CNTQADTKVCGCTQEQHPTC-----EECKECDECKQCKACLVQ 484

RESULT 15
S78549
notch3 protein - human
C:Species: Homo sapiens (man)
C:Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004
C:Accession: S78549; S71825
R:Joutel, A.; Tournier-Lasserre, E.
submitted to the EMBL Data Library, April 1997
A:Reference number: S78549
A:Accession: S78549
A:Molecule type: mRNA
A:Residues: 1-2321 <JOU1>
A:Cross-references: UNIPROT:Q9UM47; UNIPARC:UPI000011D827; EMBL:U97669; NID:g2668591; PI
R:Joutel, A.; Corpechot, C.; Ducros, A.; Vahedi, K.; Chabrier, H.; Mouton, P.; Alamowicz
X, M.M.; Weissenbach, J.; Bach, J.F.; Bousser, M.G.; Tournier-Lasserre, E.
Nature 383, 707-710, 1996
A:Title: Notch3 mutations in CADASIL, a hereditary adult-onset condition causing stroke
A:Reference number: S71825; PMID:97032728; PMID:8878478
A:Accession: S71825
A>Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 67-113;138-194;268-333,'G',335-346;536-613;716-765;1240-1279;1815-1888 <JOU2>
A:Cross-references: UNIPARC:UPI0000177457; UNIPARC:UPI0000177458; UNIPARC:UPI0000177459;
C:Genetics:
A:Gene: notch3
A:Map position: 19p13.1
C:Function:
A:Description: may be involved in pathogenesis of CADASIL, causing a type of stroke and
C:Superfamily: notch protein; ankyrin repeat homology; EGF homology
C:Keywords: tandem repeat; transmembrane protein
F:123-155/Domain: EGF homology <EGX1>
F:162-194/Domain: EGF homology <EGF1>
F:240-271/Domain: EGF homology <EGX2>
F:318-349/Domain: EGF homology <EGF>
F:473-504/Domain: EGF homology <EGX3>
F:853-884/Domain: EGF homology <EGF3>
F:928-959/Domain: EGF homology <EGX4>
F:1838-1870/Domain: ankyrin repeat homology <AN1>
F:1871-1903/Domain: ankyrin repeat homology <AN2>
F:1905-1937/Domain: ankyrin repeat homology <AN3>
F:1938-1970/Domain: ankyrin repeat homology <AN4>
F:1971-2003/Domain: ankyrin repeat homology <AN5>

Query Match 5.2%; Score 110; DB 2; Length 2321;

Best Local Similarity 22.1%; Pred. No. 1.3;
Matches 78; Conservative 35; Mismatches 150; Indels 90; Gaps 21;

QY 41 CTQARRKCEANPACAAAYQHLSGCTSSLSRPLPLEESAMADCLAAEQRLNSLID-CR 99
DB 542 CDRNVDDCSPPC-----HHGRCVDGI-----ASFSCACAPGYTGTTRCESQVDECR 587

QY 100 CHRRMKHQATCLDI---YVTHVHPARSLG-DYELDVSPYEDTTSKPKMNLKLNMLKPD 155
DB 588 -SOPCRHGGKCLDLVDKYLRCRCPSTGTTGVNCEVNI-----DDCASNPCTFGVCRDGINRYD 642

QY 156 SCLCLK--FAMLCCLTLH-DKCDRLRKAYGEAC-----SGIRC-----QRHLCLAQLRSFFE 202
DB 643 C-VCQPGFTGPLCNVEINECASSPCGEGGSCVDGNGFCLCPGPGSLPPLCLPPSHPCA 701

QY 203 KAAESH-----AOGLLLCPCAPEDAGCGRRRRNTIAPSCALPSVTNCLDLRSFCRADPL 257
DB 702 EPC-SHGICYDAPGGPRCVCBPGWSG-----PRCSQSILARDACES--QPCRAGGT 748

QY 258 CFSRLMDFQTHCHP-----MDILGTCA-----EQSRCL 286
DB 749 CSSDGMGFHCTCPPGVQGRQCELLSPCTNPCEHGGRCESAPGQLPVCSPQGWQGRPCQ 808

QY 287 RAYLGLIGTA-MTPNFIKSVNTTVALSCTCRGSNQLQDECEQLERSFSQNPCL 338
DB 809 QDVDECAGPAPCGPHGIC-TNLGASFSCCTCHG-GYTGPSCDODINDCDENPCL 859

Search completed: May 12, 2006, 02:10:30
Job time : 27.404 secs

GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 12, 2006, 02:00:03 ; Search time 152.922 Seconds
(without alignments)
1831.616 Million cell updates/sec

Title: US-10-668-936-17
Perfect score: 2131
Sequence: 1 MGLSWSPRPPLMLLLVLS.....PRLPILSFSILPILLQLTW 397

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2131	100.0	397	1	GFR3_MOUSE
2	2058	96.6	385	2	Q9R2D0_MOUSE
3	1972	92.5	397	2	Q6AXR3_RAT
4	1646.5	77.3	400	1	GFR3_HUMAN
5	1167	54.8	222	2	Q9Q2G2_RAT
6	581.5	27.3	465	1	GFR22_CHICK
7	577.5	27.1	444	2	Q792X9_RAT
8	577.5	27.1	464	2	Q5B9X0_BOVIN
9	577.5	27.1	464	2	Q35977_RAT
10	576.5	27.1	463	1	GFR2_MOUSE
11	576.5	27.1	463	2	Q920Y3_MOUSE
12	574.5	27.0	460	2	Q5R229_PONPY
13	574.5	27.0	464	1	GFR22_HUMAN
14	574.5	27.0	464	2	Q6GTR9_HUMAN
15	574.5	27.0	464	2	Q5RAD6_PONPY
16	564.5	26.5	464	2	Q5R9T3_PONPY
17	531	24.9	469	1	GFR1_CHICK
18	519	24.4	495	2	Q6T5C3_BRARE
19	514.5	24.1	481	2	Q98T78_BRARE
20	513.5	24.1	465	1	GFR1_HUMAN
21	513	24.1	472	2	Q98T79_BRARE
22	510	23.9	463	2	Q35252_MOUSE
23	508.5	23.9	468	1	GFR1_MOUSE
24	508.5	23.9	468	2	Q35246_MOUSE
25	507	23.8	431	2	Q4R568_TETNG
26	507	23.8	463	2	Q35748_RAT
27	505.5	23.7	468	1	GFR1_RAT
28	490	23.0	431	1	GFR4_CHICK
29	489.5	23.0	484	2	Q4S1R4_TETNG
30	468.5	22.0	333	2	Q4RTG0_TETNG
31	442.5	20.8	358	2	Q922A3_MOUSE

32	436.5	20.5	359	2	Q58J92_HUMAN	Q58j92 homo sapien
33	429.5	20.2	342	2	Q4SDM1_TETNG	Q4sdm1 tetraodon n
34	429	20.1	330	2	Q922A2_MOUSE	Q922a2 mus musculus
35	412	19.3	203	2	Q4SF7_TETNG	Q4sf7 tetraodon n
36	375.5	17.6	260	1	GFR4_MOUSE	Q9jft2 mus musculus
37	371	17.4	273	1	GFR4_RAT	Q9ep12 rattus norv
38	294	13.8	299	1	GFR4_HUMAN	Q9gz27 rattus norv
39	294	13.8	299	2	Q5JT74_HUMAN	Q5jt74 homo sapien
40	272.5	12.8	247	2	Q4SG83_TETNG	Q4sg83 tetraodon n
41	264.5	12.4	182	2	Q5JT77_HUMAN	Q5jt77 homo sapien
42	232	10.9	394	2	Q6UXV0_HUMAN	Q6uxv0 homo sapien
43	223.5	10.5	333	2	Q6SJE0_MOUSE	Q6sjeo mus musculus
44	204	9.6	223	2	Q9QWK2_MOUSE	Q9qwk2 mus musculus
45	199.5	9.4	109	2	Q8JG58_AMBME	Q8jg58 ambystoma m

ALIGNMENTS

RESULT 1

GFR3_MOUSE STANDARD; PRT; 397 AA.

AC Q35118: Q35325; Q55243; Q6NZC2; Q8C8L9;

DT 25-OCT-2004 (Rel. 45, Created)

DT 25-OCT-2004 (Rel. 45, Last sequence update)

DT 10-MAY-2005 (Rel. 47, Last annotation update)

DE GDNF family receptor alpha 3 precursor (GFR-alpha 3) (GFRalpha3).

GN Name=Gfra3;

OS Mus musculus (Mouse);

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Theria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

OC Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6; TISSUE=Heart;

RX MEDLINE=98205811; PubMed=9535755; DOI=10.1006/bbrc.1998.8361;

RA Nomoto S., Ito S., Yang L.-X., Kiuchi K.;

RT "Molecular cloning and expression analysis of GFR alpha-3, a novel cDNA related to GDNF alpha and NTR-alpha.";

RL Biochem. Biophys. Res. Commun. 244:849-853(1998).

RN [2]

RP NUCLEOTIDE SEQUENCE.

RX MEDLINE=98420233; PubMed=9749804;

RA Widenfalk J., Tomac A., Lindqvist E., Hoffer B., Olson L.;

RT "GFRalpha-3, a protein related to GFRalpha-1, is expressed in developing peripheral neurons and ensheathing cells.";

RL Eur. J. Neurosci. 10:1508-1517(1998).

RN [3]

RP NUCLEOTIDE SEQUENCE.

RX PubMed=9448325; DOI=10.1073/pnas.95.3.1295;

RA Naveilhan P., Baudet C., Mikaelis A., Shen L., Westphal H., Ernfor P.;

RT "Expression and regulation of GFRalpha3, a glial cell line-derived neurotrophic factor family receptor.";

RL Proc. Natl. Acad. Sci. U.S.A. 95:1295-1300(1998).

RN [4]

RP NUCLEOTIDE SEQUENCE.

RX MEDLINE=98245162; PubMed=9576965; DOI=10.1073/pnas.95.10.5801;

RA	Baloh R.H.	Gorodinsky A., Golden J.P., Tansey M.G., Keck C.L., Popescu N.C., Johnson E.M. Jr., Milbrandt J.;	RT "GFRalpha3 is an orphan member of the GDNF/neurturin/persephin receptor family.";	RL Proc. Natl. Acad. Sci. U.S.A. 95:5801-5806(1998).	
RN	[5]		RP NUCLEOTIDE SEQUENCE.		
RX	MEDLINE=98271460; PubMed=9608533; DOI=10.1006/mcne.1998.0667;		RA Trupp M., Raynoschek C., Belluardo N., Ibanez C.F.;	RT "Multiple GFI-anchored receptors control GDNF-dependent and independent activation of the c-Ret receptor tyrosine kinase.";	
RL	Mol. Cell. Neurosci. 11:47-63(1998).		RN [6]		
RP	NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].		RX STRAIN=C57BL/6J; TISSUE=Adrenal gland;		

RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawai H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Perlea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Haashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RA "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs";
RL Nature 420:563-573 (2002).
RN [7]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC TISSUE=Pancreas;
RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D., Munz D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Richmond J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: Receptor for the glial cell line-derived neurotrophic
CC factor, artemin. Mediates the artemin-induced autophosphorylation
CC and activation of the RET receptor tyrosine kinase (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor (By
CC similarity).
CC -!- SIMILARITY: Belongs to the GDNF family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; AB008833; BAA23562.1; -; mRNA.
CC EMBL; AF041842; AAC23558.1; -; mRNA.
CC EMBL; AF036163; AAC24468.1; -; mRNA.
CC EMBL; AF051766; AAC24354.1; -; mRNA.
CC EMBL; AF020305; AAB70931.1; -; mRNA.

DR EMBL; AK046542; BAC32778.1; -; mRNA.
DR EMBL; BC066202; AAB66202.1; -; mRNA.
DR PIR; J00082; JE0082.
DR Ensemble; ENSMUSG0000024366; Mus musculus.
DR MGI; MGI:1201403; Gira3.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0008046; F:axon guidance receptor activity; IMP.
DR GO; GO:0015026; F:coreceptor activity; TAS.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0007411; F:axon guidance; IMP.
DR GO; GO:0007422; F:peripheral nervous system development; IMP.
DR GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. . ; TAS.
DR InterPro; IPR003438; GDNF_receptor.
DR InterPro; IPR003505; GDNF_receptorA3.
DR PANTHER; PTHR10269; GDNF_receptor; 1.
DR Pfam; PF02351; GDNF; 1.
DR PRINTS; PR01319; GDNFRALPHA3.
DR PRINTS; PR01316; GDNFRECEPTOR.
DR Glycoprotein; GPI-anchor; Lipoprotein; Membrane; Receptor; Signal.
KW SIGNAL 1 28 Potential.
FT CHAIN 29 371 GDNF family receptor alpha 3.
FT PROPEP 372 397 Removed in mature form (Potential).
FT LIPID 371 GPI-anchor amidated asparagine (Potential).
FT CARBOHYD 92 92 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 145 145 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 306 306 N-linked (GlcNAc. .) (Potential).
FT CONFLICT 5 6 WS -> LE (in Ref. 2 and 3).
FT CONFLICT 66 66 S -> C (in Ref. 6).
FT CONFLICT 218 218 A -> P (in Ref. 2, 3 and 5).
FT CONFLICT 314 314 T -> S (in Ref. 7).
SQ SEQUENCE 397 AA; 44307 MW; BB66CBF65D32A4B9 CRC64;
Query Match 100.0%; Score 2131; DB 1; Length 397;
Best Local Similarity 100.0%; Pred. No. 3.7e-171;
Matches 397; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGLSSPPPLLMILLVLSLWPLGAGNSLATENRFVNSCTQARKKCEANPACKAAAYQH 60
DB 1 MGLSSPPPLLMILLVLSLWPLGAGNSLATENRFVNSCTQARKKCEANPACKAAAYQH 60
QY 61 LGSCTSSLRPLPLESAMSADCLAEABQLRNSSLIDCRCHRMKHQATCLDIYWTVHPA 120
DB 61 LGSCTSSLRPLPLESAMSADCLAEABQLRNSSLIDCRCHRMKHQATCLDIYWTVHPA 120
QY 121 RSLGDIYELDVSPYETVTSKPKWNLSKLNMLKPSDLCLKEAMCTLDKCDRLRKAYG 180
DB 121 RSLGDIYELDVSPYETVTSKPKWNLSKLNMLKPSDLCLKEAMCTLDKCDRLRKAYG 180
QY 181 EACSGIRCORHLCILAQLRSFFFEKAASHAQGLLLCPACAPEDAGCGERRNTIAPSCLPS 240
DB 181 EACSGIRCORHLCILAQLRSFFFEKAASHAQGLLLCPACAPEDAGCGERRNTIAPSCLPS 240
QY 241 VTFPCNLDLRSFCRADPLCRSLRMLDFQTHCPMDIILGTCAEQSRCLRAYLGLIGTAMTNP 300
DB 241 VTFPCNLDLRSFCRADPLCRSLRMLDFQTHCPMDIILGTCAEQSRCLRAYLGLIGTAMTNP 300
QY 301 FISKVNTTVALSCTCRGSLNLODCEQLERSFSONPCLVEATAAKWRFHQLPFSQDWADS 360
DB 301 FISKVNTTVALSCTCRGSLNLODCEQLERSFSONPCLVEATAAKWRFHQLPFSQDWADS 360
QY 361 TFSVVOQNSNPALRLQPLRPILSPILPILLLQTLW 397
DB 361 TFSVVOQNSNPALRLQPLRPILSPILPILLLQTLW 397
RESULT 2
Q9R2D0_MOUSE PRELIMINARY; PRT; 385 AA.
ID Q9R2D0_MOUSE
AC Q9R2D0;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)

DE TGF-beta-related neurotrophic receptor-3 precursor.
GN Name=Gfra3; Synonyms=TrnR-3;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Swiss-Webster
RA Zhong J., Annes M., Tolle A., Heumann R.;
RT "Molecular cloning of a new member of TrnR family";
RL Submitted (Oct-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; Y15110; CAA75384.1; -; mRNA.
DR MGI; MGI:1201403; Gfra3.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0008046; F:axon guidance receptor activity; IMP.
DR GO; GO:0015026; F:coreceptor activity; TAS.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0007411; P:axon guidance; IMP.
DR GO; GO:0007422; P:peripheral nervous system development; IMP.
DR GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. . .; TAS.
DR InterPro; IPR003438; GDNF_receptor.
DR InterPro; IPR003505; GDNF_receptorA3.
DR Pfam; PF02351; GDNF; 1.
DR PRINTS; PR01319; GDNFRALPHA3.
DR PRINTS; PR01316; GDNFRECEPTOR.
KW Receptor; Signal.
FT SIGNAL 1 15 Potential.
SQ SEQUENCE 385 AA; 42997 MW; 91A7F3F9FF30ED14 CRC64;

Query Match 96.6%; Score 2058; DB 2; Length 385;
Best Local Similarity 99.7%; Pred. No. 5.2e-165;
Matches 384; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 13 MILLVLSLWPLPLGAGNSLATENRFVNSCTQARKKCEANPACKAAYQHLGSCSTSSLSRPL 72
Db 1 MILLVLSLWPLPLGAGNSLATENRFVNSCTQARKKCEANPACKAAYQHLGSCSTSSLSRPL 60

Qy 73 PLESAMSDCLEAABQRLNSLLDCRHRMKHQATCLDIYVTVHPARSLGDELVDSP 132
Db 61 PLESAMSDCLEAABQRLNSLLDCRHRMKHQATCLDIYVTVHPARSLGDELVDSP 120

Qy 133 YEDVTSTKPKWKNLSKLNMLKPDSDCLCKFAMLTCLHDKCDRLKAYGEACSGIRCQRL 192
Db 121 YEDVTSTKPKWKNLSKLNMLKPDSDCLCKFAMLTCLHDKCDRLKAYGEACSGIRCQRL 180

Qy 193 CLAQLRSFFFEKAABSHAGQLLLCPAPEDAGCGRRRNTTAPSCALPSVTPNCLDLRSFC 252
Db 181 CLAQLRSFFFEKAABSHAGQLLLCPAPEDAGCGRRRNTTAPSCALPSVTPNCLDLRSFC 240

Qy 253 RADPLCSRLMDFTQCHPMDILGTCTATEOSRCLRAYLIGLTAMTNPFIKVNNTVALS 312
Db 241 RADPLCSRLMDFTQCHPMDILGTCTATEOSRCLRAYLIGLTAMTNPFIKVNNTVALS 300

Qy 313 CTCRGSNLDQECQLRSFQNPCLVEAIAAKRFRQLFSQDWDSTFVVQQQNSNP 372
Db 301 CTCRGSNLDQECQLRSFQNPCLVEAIAAKRFRQLFSQDWDSTFVVQQQNSNP 360

Qy 373 ALRLQPLRLPILSPILPILLOTI 397
Db 361 ALRLQPLRLPILSPILPILLOTI 385

RESULT 3
Q6AXR3 RAT PRELIMINARY; PRT; 397 AA.
ID Q6AXR3 RAT PRELIMINARY; PRT; 397 AA.
AC Q6AXR3;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Glial cell line derived neurotrophic factor family receptor alpha 3.

GN Name=Gfra3;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Kidney;
RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Srausberg R.L., Reingold E.A., Grouse L.H., Derge J.G.
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Kidney;
RC NTH MGC Project;
RL Submitted (Aug-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC079378; AAH79378.1; -; mRNA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR003438; GDNF_receptor.
DR InterPro; IPR003505; GDNF_receptorA3.
DR Pfam; PF02351; GDNF; 1.
DR PRINTS; PR01319; GDNFRALPHA3.
DR PRINTS; PR01316; GDNFRECEPTOR.
KW Receptor.
SQ SEQUENCE 397 AA; 44053 MW; E11D2E7B9CB46AF8 CRC64;

Query Match 92.5%; Score 1972; DB 2; Length 397;
Best Local Similarity 92.9%; Pred. No. 9.6e-158;
Matches 369; Conservative 9; Mismatches 19; Indels 0; Gaps 0;

Qy 1 MGLSWSRPPRLMILLVLSLWPLPLGAGNSLATENRFVNSCTQARKKCEANPACKAAYQH 60
Db 1 MGLSWSRPPRLVILLVLSLWPLPLGAGNSLATENRFVNSCTQARKKCEANPACKAAYQH 60

Qy 61 LGSCTSSLSRPLPLESAMSDCLEAABQRLNSLLDCRHRMKHQATCLDIYVTVHPA 120
Db 61 LDSCTPSLSPLPSGESATSAACLEAAQRLNSLLDCRHRMKHQATCLDIYVTVHPV 120

Qy 121 RSLGDIYELVDSPYEDVTSTKPKWKNLSKLNMLKPDSDCLCKFAMLTCLHDKCDRLKAYG 180
Db 121 RSLGDIYELVDSPYEDVTSTKPKWKNLSKLNMLKPDSDCLCKFAMLTCLHDKCDRLKAYG 180

Qy 181 EACSGIRCQRLHCLAQRLSFFFEKAABSHAGQLLLCPAPEDAGCGRRRNTTAPSCALPS 240
Db 181 EACSGIRCQRLHCLAQRLSFFFEKAABSHAGQLLLCPAPEDAGCGRRRNTTAPSCALPS 240

Qy 241 VTPNCLDLRSFCRADPLCSRLMDFTQCHPMDILGTCTATEOSRCLRAYLIGLTAMTNP 300
Db 241 VAPNCLDLRSFCRADPLCSRLMDFTQCHPMDILGTCTATEOSRCLRAYLIGLTAMTNP 300

Qy 301 FISKVNNTVALSCTCRGSNLDQECQLRSFQNPCLVEAIAAKRFRQLFSQDWDSTFVVQQQNSNP 360
Db 301 FISKVNNTVALGCTCRGSNLDQECQLRSFQNPCLVEAIAAKRFRQLFSQDWDSTFVVQQQNSNP 360

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QY 361 TFSVVOQNSPALRLOPRLPILSFILPILLOTLW 397
DB 361 TFSVMOQNSPALRLOPRLPVLSPFILTLLOTLW 397

RESULT 4
GFR3_HUMAN
ID GFR3_HUMAN STANDARD; PRT; 400 AA.
AC O60609; Q6UW20; Q8IU22;
DT 16-OCT-2004 (Rel. 40, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE GDNF family receptor alpha 3 precursor (GFR-alpha 3) (GFRalpha3).
GN Name=GFR3; ORFNames=UNQ339/PRO538/PRO3664;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;

[1]
RN NUCLEOTIDE SEQUENCE (ISOFORM 1), AND TISSUE SPECIFICITY.
RP MEDLINE=98245162; PubMed=9576965; DOI=10.1101/gr.1293003;
RX Baloh R.H., Gorodinsky A., Golden J.P., Tansey M.G., Keck C.L.,
RA Popescu N.C., Johnson E.M. Jr., Milbrandt J.;
RT "GFRalpha3 is an orphan member of the GDNF/neurturin/persephin
RT receptor family.";
RL Proc. Natl. Acad. Sci. U.S.A. 95:5801-5806 (1998).
[2]
RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORMS 1 AND 2).
RP MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RX Clark H.F., Gurney A.B., Abaya E., Baker K., Baldwin D.T., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J.S., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M.R., Robbie E., Sanchez C., Schoenfeld J.,
RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vandlen R.L., Watanabe C., Wleand D., Woods K., Xie M.-H.,
RA Yansura D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A.D.,
RA Wood W.I., Godowski P.J., Gray A.M.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment.";
RL Genome Res. 13:2265-2270(2003).
[3]
RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).
RP TISSUE=Pancreas;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Dege J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Tohiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Guaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Heiton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smillius D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[4]
RN PROTEIN SEQUENCE OF 32-46.
RP PubMed=15340161; DOI=10.1110/ps.04682504;
RX Zhang Z., Henzel W.J.;
RT "Signal peptide prediction based on analysis of experimentally
RT verified cleavage sites.";

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RL Protein Sci. 13:2819-2824 (2004).
RN [5]
RX FUNCTION.
RX MEDLINE=99098192; PubMed=9883723; DOI=10.1016/S0896-6273(00)80649-2;
RA Baloh R.H., Tansey M.G., Lampe P.A., Fahrner T.J., Enomoto H.,
RA Simburger K.S., Leitner M.L., Araki T., Johnson E.M. Jr.,
RA Milbrandt J.;
RT "Artemin, a novel member of the GDNF ligand family, supports
RT peripheral and central neurons and signals through the GFRalpha3-RET
RT receptor complex.";
RL Neuron 21:1291-1302(1998).
CC -!- FUNCTION: Receptor for the glial cell line-derived neurotrophic
CC factor, artemin. Mediates the artemin-induced autophosphorylation
CC and activation of the RET receptor tyrosine kinase.
CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=O60609-1; Sequence=Displayed;
CC Name=2;
CC IsoId=O60609-2; Sequence=VSP_010942;
CC -!- TISSUE SPECIFICITY: Widely expressed in adult and fetus which
CC exhibit a similar pattern. Essentially not expressed in the
CC central nervous system, but highly expressed in several sensory
CC and sympathetic ganglia of the peripheral nervous system. Moderate
CC expression in many nonneural tissues, particularly those of the
CC digestive and urogenital systems, but high expression in stomach
CC and appendix. Several types of glandular tissues show low
CC expression. Very low or no expression detected in the
CC hematopoietic system.
CC -!- SIMILARITY: Belongs to the GDNFR family.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; AF051767; AAC24355.1; -; mRNA.
CC EMBL; AY358997; AAQ89356.1; -; mRNA.
CC EMBL; AY359037; AAQ89396.1; -; mRNA.
CC EMBL; BC037951; AAH37951.1; -; mRNA.
CC Ensembl; ENSG00000146013; Homo sapiens.
CC HGNC; HGNC:4245; GFR3.
CC MIM; 605710; -.
CC GO; GO:0019898; C:extrinsic to membrane; TAS.
CC GO; GO:0005102; F:receptor binding; TAS.
CC GO; GO:0007422; P:peripheral nervous system development; TAS.
CC GO; GO:0007165; P:signal transduction; TAS.
CC InterPro; IPR003438; GDNF_receptor.
CC InterPro; IPR003505; GDNF_receptorA3.
CC PANTHER; PTHR10269; GDNF_receptor; 1.
CC Pfam; PF02351; GDNF; 1.
CC PRINTS; PR01319; GDNFRALPHA3.
CC PRINTS; PR01316; GDNFRECEPTOR.
CC Alternative splicing: Direct protein sequencing; Glycoprotein;
CC GPI-anchor; Lipoprotein; Membrane; Receptor; Signal.
CC SIGNAL 1 31
CC CHAIN 32 374 GDNF family receptor alpha 3.
CC PROPEP 375 400 Removed in mature form (Potential).
CC LIPID 374 374 GPI-anchor amidated asparagine
CC (Potential).
CC CARBOHYD 95 95 N-linked (GlcNAc...) (Potential).
CC CARBOHYD 148 148 N-linked (GlcNAc...) (Potential).
CC CARBOHYD 309 309 N-linked (GlcNAc...) (Potential).
CC VARSPLIC 127 157 Missing (in isoform 2).
CC /FTId=VSP_010942.
CC FT CONFLICT 108 108 K -> R (in Ref. 1).
CC SEQUENCE 400 AA; 44511 MW; B0BC252FE1F072C7 CRC64;

```

Query Match 77.3%; Score 1646.5; DB 1; Length 400;
Best Local Similarity 77.8%; Pred. No. 2.7e-130;
Matches 305; Conservative 30; Mismatches 56; Indels 1; Gaps 1;

QY 7 PRPP-LLMILLVLSLWPLGAGNSLATENRFVNSCTOARKKCEANPACKAAYOHLGSGT 65
 DB 9 PLPPVWMLLLPPSLPLAAGDPPTESRLMNSCLQARRKQADPTCSAAYHLLDST 68
 QY 66 SSLSRPLPESAMSADCLAEABQLRNSLLIDCHRRMKHQATCLDIYTWVHPARSLGD 125
 DB 69 SSIITPLPSEEPADCLAEAAQRLNSLLIGCMCHRRMKQVACLDIYTWVHARSIGN 128
 QY 126 YELDVSPYEDVTSPKPKWNLKLNMLKPDSDCLKPFAMLTCTLDKCDRLRKAYGEACSG 185
 DB 129 YELDVSPYEDVTSPKPKWNLKLNMLKPDSDCLKPFAMLTCTLDKCDRLRKAYGEACSG 188
 QY 186 IRCORHCLAQIRFFFEKAAESHAQGLLLCPAPEDAGCGERRRNTIAPSCALPVSVPNC 245
 DB 189 PHCQRHVLCRLQTLFFFEKAAESHAQGLLLCPAPEDAGCGERRRNTIAPNCALPVPVNC 248
 QY 246 LDLSRPFCEADPLCRSLRMDFOHCHPMDILGTCTEQSRCLRAYLGLIGTAMTNPFSKV 305
 DB 249 LELRLCFSDPLCRSLRMDFOHCHPMDILGTCTEQSRCLRAYLGLIGTAMTNPFSNV 308
 QY 306 NTTVALSCTCGSGNLODECQLERSFSONPCLVEATAAKWRFHQRLFSQDWDSTFSV 365
 DB 309 NTSVALSCTCGSGNLODECQEMLEGGFHSNCPCLTEATAAKWRFHQRLFSQDWDPTFAV 368
 QY 366 QQONSFPALRLQPLPILSILPILQLTLW 397
 DB 369 AHQENPAVRPQPVPSLFSCTLPILLLSLW 400

RESULT 5

Q9QZG2 RAT .PRELIMINARY; PRT; 222 AA.
 AC Q9QZG2;
 DT 01-MAY-2000 (TRENBLrel. 13, Created)
 DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
 DE GDNF-family, receptor alpha 3 (Fragment).
 GN Name=Gfra3; Synonyms=Gfra3-3;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Rattus.
 OC NCBI_TaxID=10116;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Sprague-Dawley; TISSUE=Cochlea;
 RX MEDLINE=20185640; PubMed=10719212; DOI=10.1016/S0169-328X(99)00328-9;
 RA Stover T., Gong T.L., Cho Y., Altschuler R.A., Lomax M.I.;
 RT "Expression of the GDNF family members and their receptors in the
 mature rat cochlea."
 RL Brain Res. Mol. Brain Res. 76:25-35(2000).
 DR ENBL; AF184920; AAF01242.1; -; mRNA.
 DR Ensembl; ENSRNOG0000020309; Rattus norvegicus.
 DR RGD; 620502; Gfra3.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR InterPro; IPR003438; GDNF receptor.
 DR InterPro; IPR003505; GDNF_receptorA3.
 DR Pfam; PF02351; GDNF; 1.
 DR PRINTS; PR01319; GDNFALPHA3.
 DR PRINTS; PR01316; GDNFRECEPTOR.
 KW Receptor.
 FT NON_TER 1 1
 FT NON_TER 222 222
 FT NON_TER 222 222
 SQ SEQUENCE 222 AA; 24791 MW; A9610F6462468C74 CRC64;
 Query Match 54.8%; Score 1167; DB 2; Length 222;
 Best Local Similarity 96.4%; Pred. No. 3.8e-90;
 Matches 214; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
 QY 136 TVTSPKPKWNLKLNMLKPDSDCLKPFAMLTCTLDKCDRLRKAYGEACSGIRCORHLCLA 195
 DB 1 TVTSPKPKWNLKLNMLKPDSDCLKPFAMLTCTLDKCDRLRKAYGEACSGIRCORHLCLA 60

QY 196 QLSRFFFEKAAESHAQGLLLCPAPEDAGCGERRRNTIAPSCALPVSVPNCILDRSFCRAD 255
 DB 61 QLSRFFFEKAAESHAQGLLLCPAPEDAGCGERRRNTIAPSCALPVSVPNCILDRSFCRAD 120
 QY 256 PLCRSLRMDFOHCHPMDILGTCTEQSRCLRAYLGLIGTAMTNPFSKVNTTVALSCTC 315
 DB 121 PLCRSLRMDFOHCHPMDILGTCTEQSRCLRAYLGLIGTAMTNPFSKVNTTVALSCTC 180
 QY 316 RGSNLODECQLERSFSONPCLVEATAAKWRFHQRLFSQDW 357
 DB 181 RGSNLODECQLEKSFSONPCLMEATAAKWRFHQRLFSQDW 222

RESULT 6
 GFRA2 CHICK STANDARD; PRT; 465 AA.
 AC O13157;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE GDNF family receptor alpha 2 precursor (GFR-alpha 2) (Neurturin
 receptor alpha) (NTRN-alpha) (NRTNR-alpha) (GDNF receptor beta)
 DE (GDNFR-beta).
 GN Name=GFRA2; Synonyms=GDNFRB;
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
 OC Gallus.
 OC NCBI_TaxID=9031;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Brain;
 RX MEDLINE=97336104; PubMed=9192899; DOI=10.1038/42729;
 RA Buj-Bello A., Adu J., Pinon L.G.P., Horton A., Thompson J.,
 RA Rosenthal A., Chinchetru M., Buchman V.L., Davies A.M.;
 RT "Neurturin responsiveness requires a GPI-linked receptor and the Ret
 receptor tyrosine kinase."
 RL Nature 387:721-724(1997).
 CC -I- FUNCTION: Receptor for neurturin. Mediates the NRTN-induced
 autophosphorylation and activation of the RET receptor. Also able
 to mediate GDNF signaling through the RET tyrosine kinase receptor
 (by similarity).
 CC -I- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
 CC -I- SIMILARITY: Belongs to the GDNFR family.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use as long as its content is in no way modified and this statement is not
 removed.
 CC -----
 CC ENBL; U90542; AAB61571.1; -; mRNA.
 DR Ensembl; ENSGALG0000001795; Gallus gallus.
 DR InterPro; IPR003438; GDNF receptor.
 DR InterPro; IPR003504; GDNF_receptorA2.
 DR PANTHER; PTHR10269; GDNF_receptor; 1.
 DR Pfam; PF02351; GDNF; 1.
 DR PRINTS; PR01318; GDNFALPHA2.
 DR PRINTS; PR01316; GDNFRECEPTOR.
 KW Glycoprotein; GPI-anchor; Lipoprotein; Membrane; Receptor; Signal.
 FT SIGNAL 1 21
 FT CHAIN 22 445
 FT PROPEP 445 465
 FT LIPID 445 445
 FT CARBOHYD 355 355
 FT CARBOHYD 387 387
 FT CARBOHYD 412 412
 SQ SEQUENCE 465 AA; 51909 MW; 22CD9024ED971F06 CRC64;
 Query Match 27.3%; Score 581.5; DB 1; Length 465;
 Best Local Similarity 36.0%; Pred. No. 2.1e-40;
 Matches 130; Conservative 51; Mismatches 135; Indels 45; Gaps 11;

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QY 41 CTQARKKCEANPACKAAYQHGLGCTSSLSRPLPLEESAMSDCLEAAEQLRNSSLIDCRC 100
DB 40 CIRANKLCAAEAGSCSSRYRTLQCLAGDRDNTML-----ANKECOAALEVLQESPLYDCRC 95
QY 101 HRRMKHQATCLDIYVTHVPARSGLDYELDVSPYEDTVTSKPWKNLSKLNML-----152
DB 96 KRGMKKEIQCLQVYNSIHGLAGEEYFYEASPYE--PITSR-----LSDIFRLASIFSGND 149
QY 153 ----KPSDILCLFAMLCITLHDKCDRLRKAYGEACS-----GIRCQRLHCLLAQLRSPFE 202
DB 96 KRGMKKEIQCLQVYNSIHGLAGEEYFYEASPYE--PITSR-----LSDIFRLASIFSGND 149
QY 153 ----KPSDILCLFAMLCITLHDKCDRLRKAYGEACS-----GIRCQRLHCLLAQLRSPFE 202
DB 150 TDPVSTVSKNCHLDAKACNLNDNCKLRSSVISICNREISPTERCNRKCHKALRQFPD 209
QY 203 KAAESHAQGLLCPCAPEDAGCGERRNTIAPSCAL-PSVTPNCLDLRSFCRADPLCRSR 261
DB 150 PATNSKNHCLDAKACNLNDNCKLRSGVISTCSKEISATEHCSRRKCHKALRQFPD 209
QY 205 ARSHAQGLLCPCAPEDAGCGERRNTIAPSCAL-PSVTPNCLDLRSFCRADPLCRSR 263
DB 210 PSEYTYRLLFCSC--KDQACAEPRRTIIPFCSYEDKEKPNCLDLRNVCRADHLCKSLA 267
QY 264 DFQTHCH-PMDILGTCTAQ-SCLRAYLGLIGTAMTNPFIKVNITVALS--CTCRSG 319
DB 268 DFHANCQASFSQTSFCPDNYQACLSYGLIGFDMTPNVDASTIITISPCSKSG 327
QY 320 NLQDECEQLERSFSONPCLVEAIAAKRPHRQLFSQDNADSTFSVVQQNSNPALRLOPR 379
DB 328 NLEEECEKFLRDTFENPCLRNAI-----QAFNGTGVNLSPKNPPPTMLPK 375
QY 380 L 380
DB 376 V 376

RESULT 7
ID Q792X9_RAT PRELIMINARY; PRT; 444 AA.
AC Q792X9;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE GDNF receptor-beta (Fragment).
GN Names=Gifra2;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Hippocampus;
RX MEDLINE=97402208; PubMed=9259272; DOI=10.1093/hmg/6.6.1267;
RA Suvanto P., Wartiovaara K., Lindahl M., Arumae U., Moshnyakov M.,
RA Horelli-Kuitunen N., Airaksinen M.S., Palotie A., Sariola H.,
RA Saarala M.;
RT "Cloning, mRNA distribution and chromosomal localisation of the gene
RT for glial cell line-derived neurotrophic factor receptor beta, a
RT homologue to GDNF-alpha."
RL Hum. Mol. Genet. 6:1267-1273 (1997).
DR EMBL; AF003825; AAD09310.1; -; mRNA.
DR GD; 61809; Gifra2.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR003438; GDNF receptor.
DR InterPro; IPR003504; GDNF_receptorA2.
DR Pfam; PF02351; GDNF; 1.
DR PRINTS; PR01318; GDNFRALPHA2.
DR PRINTS; PR01316; GDNFRECEPTOR.
KW Receptor.
FT NON TER
SQ SEQUENCE 444 444
Query Match 444 444
Best Local Similarity 44.4 AA; A548644EDB36D5F3 CRC64;
Matches 127; Conservative 40; Mismatches 125; Indels 35; Gaps 9;

QY 41 CTQARKKCEANPACKAAYQHGLGCTSSLSRPLPLEESAMSDCLEAAEQLRNSSLIDCRC 100

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DB 40 CVRANELCAESNCSSRYRTLQCLAGDRDNTML-----ANKECOAALEVLQESPLYDCRC 95
QY 101 HRRMKHQATCLDIYVTHVPARSGLDYELDVSPYEDTVTSKPWKNLSKLNML-----152
DB 96 KRGMKKEIQCLQVYNSIHGLAGEEYFYEASPYE--PITSR-----LSDIFRLASIFSGTG 149
QY 153 ----KPSDILCLFAMLCITLHDKCDRLRKAYGEACS-----GIRCQRLHCLLAQLRSPFE 202
DB 150 TDPVSTVSKNCHLDAKACNLNDNCKLRSSVISICNREISPTERCNRKCHKALRQFPD 209
QY 203 KAAESHAQGLLCPCAPEDAGCGERRNTIAPSCAL-PSVTPNCLDLRSFCRADPLCRSR 261
DB 210 RVPSEYTYRMLFCSC--QDQACAEPRRTIIPFCSYEDKEKPNCLDLRSLCRTLHLCSR 267
QY 262 LMDFOPTHCH--MDILGTCTAQEQSCLRAYLGLIGTAMTNPFIKVNITVALS--CTCRG 317
DB 268 LADFHFANCRASYRTITSPADNYQACLSYAGMIGDMTPNVDNSTPNTGIVVSPWCNCRG 327
QY 318 SGNLQDECEQLERSFSONPCLVEAIAA 344
DB 328 SGNMEECEKFLRDTFENPCLRNAIQA 354

RESULT 8
QSE9X0_BOVIN PRELIMINARY; PRT; 464 AA.
ID QSE9X0;
AC QSE9X0;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE GDNF family receptor alpha 2 preproprotein.
GN Name=GPR2;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Pooled;
RX MEDLINE=21180013; PubMed=11282978; DOI=10.1101/gr.170101;
RA Smith T.P.L., Grosse W.M., Freking B.A., Roberts A.J., Stone R.T.,
RA Casas E., Wray J.E., White J., Cho J., Fahrenkrug S.C., Bennett G.L.,
RA Heaton M.P., Laegreid W.W., Rohrer G.A., Chitko-McKown C.G.,
RA Perteau G., Holt I., Karamycheva S., Liang F., Quackenbush J.,
RA Keele J.W.;
RT "Sequence evaluation of four pooled-tissue normalized bovine CDNA
RT libraries and construction of a gene index for cattle."
RL Genome Res. 11:626-630 (2001).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Pooled;
RA Harhay G.P., Sonstegard T.S., Clawson M.L., Heaton M.P., Keele J.W.,
RA Snelling W.M., Weidmann R.T., Smith T.P.L.;
RT "Sequencing and analysis of Bos taurus full-length insert cDNA
RT clones."
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BT020800; AX08817.1; -; mRNA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR003438; GDNF receptor.
DR InterPro; IPR003504; GDNF_receptorA2.
DR Pfam; PF02351; GDNF; 1.
DR PRINTS; PR01318; GDNFRALPHA2.
DR PRINTS; PR01316; GDNFRECEPTOR.
KW Receptor.
SQ SEQUENCE 464 AA; 51658 MW; BF0BF88F429985AA CRC64;

Query Match 27.1%; Score 577.5; DB 2; Length 464;
Best Local Similarity 37.9%; Pred. No. 4.6e-40;
Matches 124; Conservative 44; Mismatches 124; Indels 35; Gaps 9;

QY 41 CTQARKKCEANPACKAAYQHGLGCTSSLSRPLPLEESAMSDCLEAAEQLRNSSLIDCRC 100

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Db 40 CVRANELCAESNCSSRYRTLRQCLAGDRNTML-----ANKECOAALEVLQESPLYDCRC 95
Qy 101 HRRMKHQATCLDIYVHTVHPARSLGVDYELDVSPYEDVTTSKPKWNLSKLNML----- 152
Db 96 KRGKKELQCLQIYWSIHLGLTEGEFEYASPYE-----PVTARLSIDIFLASIFSGTG 149
Qy 153 -----KPSDILCLKPFAMCTLHDKCDRLRKAYGEACS-----GIRCQRHLCLAQLRSFFE 202
Db 150 ADPAVSTKSNHCLDAKACNLNDCKLRSSYSISICNREISPTERCNRRKCHKALRQFFD 209
Qy 203 KAASHAQGLLCPACEDAGCGRRNTIAPSCAL-PSVTPNCLDLRSFCRADPLCRSR 261
Db 210 RVPSEYTYRMLFCSC--QDQACARRRQTLIPSCSYEDKEKPNCLDLRSCLRTDHLCRSR 267
Qy 262 LMDFOETHCH-PMDILGTGTCATEQ-SRCLRAYLGLGTAMTNFISKVNTTVALS--CTCRG 317
Db 268 LADFHANCRAASYQVLTSCPTDNYQACLSYAGMIGFDITPNYDSSPTGIUVSPWCSCRG 327
Qy 318 SGNLQDECEQLERSFSQNPLVEAIAA 344
Db 328 SGNMEECEKPLDFTENPCLRNAIQA 354

RESULT 9
O35977 RAT PRELIMINARY; PRT; 464 AA.
AC O35977;
DT 01-JAN-1998 (TriEMBLrel. 05, Created)
DT 01-JAN-1998 (TriEMBLrel. 05, Last sequence update)
DT 01-FEB-2005 (TriEMBLrel. 29, Last annotation update)
DE Glial cell line-derived neurotrophic factor receptor-beta (RET ligand 2).
DE Name=Gfra2; Synonyms=GNFR-beta, RETL2;
GN Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN NUCLEOTIDE SEQUENCE.
RP MEDLINE=9271460; PubMed=9608533; DOI=10.1006/mcne.1998.0667;
RA Trupp M., Raynoschek C., Belluardo N., Ibanez C.F.;
RA Sanicola M., Hession C.A., Worley D.S., Carmillo P., Ehrenfels C.,
RA Walus L., Robinson S., Jaworski G., Wei H., Tizard R., Whitty A.,
RA Pepinsky R.B., Cate R.L.;
RT "Glial cell line-derived neurotrophic factor-dependent RET activation can be mediated by two different cell-surface accessory proteins.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:6238-6243(1997).
DR EMBL; AF005226; AABG2247.1; -; mRNA.
DR EMBL; U97143; AAC53301.1; -; mRNA.
DR Ensembl; ENSRNOG0000014010; Rattus norvegicus.
DR RGD; 61809; Gfra2.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR003438; GDNF_receptor.
DR InterPro; IPR003504; GDNF_receptorA2.
DR Pfam; PF02351; GDNF; 1.
DR PRINTS; PR01318; GDNFRALPHA2.
DR PRINTS; PR01316; GDNFRCEPTOR.
KW Receptor.
SQ SEQUENCE 464 AA; 51668 MW; 81168301BE50D6CC CRC64;
Query Match 27.1%; Score 577.5; DB 2; Length 464;
Best Local Similarity 38.8%; Pred. No. 4.6e-40;
Matches 127; Conservative 40; Mismatches 125; Indels 35; Gaps 9;
Qy 41 CTQARKKCEANPACKAAYQHLGCTSSLSRPLPLEBSAMSADCLAEAAQLRNSLIDCRC 100

Db 40 CVRANELCAESNCSSRYRTLRQCLAGDRNTML-----ANKECOAALEVLQESPLYDCRC 95
Qy 101 HRRMKHQATCLDIYVHTVHPARSLGVDYELDVSPYEDVTTSKPKWNLSKLNML----- 152
Db 96 KRGKKELQCLQIYWSIHLGLTEGEFEYASPYE-----PVTARLSIDIFLASIFSGTG 149
Qy 153 -----KPSDILCLKPFAMCTLHDKCDRLRKAYGEACS-----GIRCQRHLCLAQLRSFFE 202
Db 150 ADPAVSTKSNHCLDAKACNLNDCKLRSSYSISICNREISPTERCNRRKCHKALRQFFD 209
Qy 203 KAASHAQGLLCPACEDAGCGRRNTIAPSCAL-PSVTPNCLDLRSFCRADPLCRSR 261
Db 210 RVPSEYTYRMLFCSC--QDQACARRRQTLIPSCSYEDKEKPNCLDLRSCLRTDHLCRSR 267
Qy 262 LMDFOETHCH-PMDILGTGTCATEQ-SRCLRAYLGLGTAMTNFISKVNTTVALS--CTCRG 317
Db 268 LADFHANCRAASYQVLTSCPTDNYQACLSYAGMIGFDITPNYDSSPTGIUVSPWCSCRG 327
Qy 318 SGNLQDECEQLERSFSQNPLVEAIAA 344
Db 328 SGNMEECEKPLDFTENPCLRNAIQA 354
RESULT 10
Gfra2 MOUSE STANDARD; PRT; 463 AA.
AC O08842;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE GDNF family receptor alpha 2 precursor (GFR-alpha 2) (Neurturin receptor alpha) (NTRN-alpha) (NRTN-alpha) (TGF-beta related neurotrophic factor receptor 2) (GDNF receptor beta) (GDNFR-beta).
DE Name=Gfra2; Synonyms=cdnfrb, Trnr2;
GN Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN NUCLEOTIDE SEQUENCE (ISOFORMS 1 AND 2).
RP MEDLINE=97325791; PubMed=9182803; DOI=10.1016/S0896-6273(00)80318-9;
RA Baloh R.H., Tansey M.G., Golden J.P., Creedon D.J., Heuckeroth R.O.,
RA Keck C.L., Zimonjic D.B., Popescu N.C., Johnson E.M. Jr.,
RA Milbrandt J.;
RT "Trnr2, a novel receptor that mediates neurturin and GDNF signaling through Ret.";
RL Neuron 18:793-802(1997).
CC -1- FUNCTION: Receptor for neurturin. Mediates the NRTN-induced autophosphorylation and activation of the RET receptor. Also able to mediate GDNF signaling through the RET tyrosine kinase receptor.
CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor (By similarity).
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1; Synonyms=Long;
CC IsoId=O08842-1; Sequence=Displayed;
CC Name=2; Synonyms=Short;
CC IsoId=O08842-2; Sequence=VSP_001662;
CC -1- TISSUE SPECIFICITY: Neurons of the superior cervical and dorsal root ganglia, and adult brain and testis. Low level in the spleen and in the adrenal gland.
CC -1- SIMILARITY: Belongs to the GDNFR family.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.
CC EMBL; AF002701; AAC53548.1; -; mRNA.

FT CONFLICT 462 462 Q -> L (in Ref. 3).
SQ SEQUENCE 464 AA; 51559 MW; 8BC604D9530FF21F CRC64;

Query Match 27.0%; Score 574.5; DB 1; Length 464;
Best Local Similarity 37.9%; Pred. No. 8.2e-40;
Matches 124; Conservative 44; Mismatches 124; Indels 35; Gaps 9;

QY 41 CTQARKKEANPACAAAYQHLSGCTSSLSRPLPLEESAMSADCLEAAEOLRNSSLIDCRC 100
DB 40 CVRANELCAAESNCSSRYRTLROCLAGDRNTWL-----ANKEQAALEVLQESPLYDCRC 95
QY 101 HRMKHQATCLDIYTWVHPARSLGDIYELDVSPYEDVTVTSPKWMNLSKL-----149
DB 96 KRGMKKELQCLQIYWSIHGLTGEFEYFVTSR-----LSDIFRLASIFSGTG 149
QY 150 --NMLKPDSDLCKPAMLCITLHDKCDRLRKAYGEACS-----GIRCORHLCLAQLRSPFE 202
DB 150 ADPVVSAKSNHCLDAKACNLNDNCKLRSSVISICNREISPTERCNRKCHKALRQFFD 209
QY 203 KAAESHAOGLLLCPACAPEDAGGERRNTIAPSCAL-PSVTPNCLDLRSFCRADPLCRSR 261
DB 210 RVPSEYTYRMLFCSC--QOQACERRRQTLFSCSYEDKEKPNCLDLRGVCRTHLCLCSR 267
QY 262 LMDFOQHCHP--MDILGTCAEQSRCLRAYLGLIGTAMTNPFIKSVNTTVALS--CTCRG 317
DB 268 LADFHANCRASTYQTVTSCPADNYQACLSGVAGMIGDMPNVDSSPTGIIVVSPWCSCRG 327
QY 318 SGNLQDECEQLERSFSQNPCLVEAIAA 344
DB 328 SGNWEECEKFLRDTFENPCLRNAIOA 354

RESULT 14

Q6GTR9 HUMAN
ID Q6GTR9_HUMAN PRELIMINARY; PRT; 464 AA.
AC Q6GTR9;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DE GDNF family receptor alpha 2, preproprotein.
GN Name=GPR2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Spatlenko M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udutin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RP NUCLEOTIDE SEQUENCE.
RN TISSUE=Brain;

RA Director MGC Project;
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL, BC041688; AAH41688.1; -, mRNA.
KW Receptor.
SQ SEQUENCE 464 AA; 51543 MW; 8BC61529530FF21F CRC64;

Query Match 27.0%; Score 574.5; DB 2; Length 464;
Best Local Similarity 37.9%; Pred. No. 8.2e-40;
Matches 124; Conservative 44; Mismatches 124; Indels 35; Gaps 9;

QY 41 CTQARKKEANPACAAAYQHLSGCTSSLSRPLPLEESAMSADCLEAAEOLRNSSLIDCRC 100
DB 40 CVRANELCAAESNCSSRYRTLROCLAGDRNTWL-----ANKEQAALEVLQESPLYDCRC 95
QY 101 HRMKHQATCLDIYTWVHPARSLGDIYELDVSPYEDVTVTSPKWMNLSKL-----149
DB 96 KRGMKKELQCLQIYWSIHGLTGEFEYFVTSR-----LSDIFRLASIFSGTG 149
QY 150 --NMLKPDSDLCKPAMLCITLHDKCDRLRKAYGEACS-----GIRCORHLCLAQLRSPFE 202
DB 150 ADPVVSAKSNHCLDAKACNLNDNCKLRSSVISICNREISPTERCNRKCHKALRQFFD 209
QY 203 KAAESHAOGLLLCPACAPEDAGGERRNTIAPSCAL-PSVTPNCLDLRSFCRADPLCRSR 261
DB 210 RVPSEYTYRMLFCSC--QOQACERRRQTLFSCSYEDKEKPNCLDLRGVCRTHLCLCSR 267
QY 262 LMDFOQHCHP--MDILGTCAEQSRCLRAYLGLIGTAMTNPFIKSVNTTVALS--CTCRG 317
DB 268 LADFHANCRASTYQTVTSCPADNYQACLSGVAGMIGDMPNVDSSPTGIIVVSPWCSCRG 327
QY 318 SGNLQDECEQLERSFSQNPCLVEAIAA 344
DB 328 SGNWEECEKFLRDTFENPCLRNAIOA 354

RESULT 15

Q5RAD6 PONPY
ID Q5RAD6_PONPY PRELIMINARY; PRT; 464 AA.
AC Q5RAD6;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DE Hypothetical protein DKFZp459C0228.
GN Name=DKFZp459C0228;
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Pongo.
OX NCBI_TaxID=9600;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Cortex;
RG The German cDNA Consortium;
RA Bloeker H., Boecher M., Brandt P., Mewes H.W., Weil B., Amid C.,
RA Osanger A., Fobo G., Han M., Wiemann S.;
RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR859081; CAH91274.1; -, mRNA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR003438; GDNF_receptor.
DR InterPro; IPR003504; GDNF_receptorA2.
DR Pfam; PF02351; GDNF; 1.
DR PRINTS; PR01318; GDNFRALPHA2.
DR PRINTS; PR01316; GDNFRECEPTOR.
KW Hypothetical protein.
SQ SEQUENCE 464 AA; 51560 MW; 46441C50299CCCFA CRC64;

Query Match 27.0%; Score 574.5; DB 2; Length 464;
Best Local Similarity 37.9%; Pred. No. 8.2e-40;
Matches 124; Conservative 44; Mismatches 124; Indels 35; Gaps 9;

QY 41 CTQARKKEANPACAAAYQHLSGCTSSLSRPLPLEESAMSADCLEAAEOLRNSSLIDCRC 100
DB 40 CVRANELCAAESNCSSRYRTLROCLAGDRNTWL-----ANKEQAALEVLQESPLYDCRC 95

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Qy 101 HRRMKHQATCLDIYVTHPARSLGDEYLDVSPYEDVTTSKPKMNLKSL----- 149
Db 96 KRGKKELQCLQIYWSIHGLTEGEEFYEAQPYE-PVTSR-----LSDIFPLASIFSGTG 149
Qy 150 --NMLKPDSDLCLKPFAMCTLHDKCDRLURKAYGEACS-----GIRCORHLCLAOIRSFPE 202
Db 150 ADPVVSAKSNHCLDAAKACNLNDNCKKLRSSYISICNREISPTERCNRRKCHKALRQFFD 209
Qy 203 KAESHAGQGLLCPAPEDAGCGRRRRNTIAPSCAL-PSVTPNCLDLRSFCRADPLCRSR 261
Db 210 RVPSEYTYRMLFCSC--ODQACABRRRROTILPSCSYEDKEKPNCLDLRGVCTDRLCRSR 267
Qy 262 LMDFTQTHCHP--MDILGTCAEQSRCLRAYLGLIGTAMTPNFISKVNTTVALS--CTCRG 317
Db 268 LADFHANCRASYQTVTSCPADNYQACLGSYAGMIGFDMTPNYVDSSPTGIWVSPWCSCRG 327
Qy 318 SGNLQDECEQLERSFSQNPCLVEAIAA 344
Db 328 SGNMEECEKFLRDFTENPCLRNAIOA 354

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Search completed: May 12, 2006, 02:09:35
Job time : 153.922 secs

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GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 12, 2006, 02:12:04 ; Search time 19.4266 Seconds
(without alignments)
959.442 Million cell updates/sec

Title: US-10-668-936-17

Perfect score: 2131

Sequence: 1 MGLSWSPRPPLMLLLVLS.....PRLPILSILPLILLQLTW 397

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 250354 seqs, 4694837 residues

Total number of hits satisfying chosen parameters: 250354

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New:

- 1: /SIDSS/ptodata/1/pubpaa/US08 NEW PUB.pep.*
- 2: /SIDSS/ptodata/1/pubpaa/US06 NEW PUB.pep.*
- 3: /SIDSS/ptodata/1/pubpaa/US07 NEW PUB.pep.*
- 4: /SIDSS/ptodata/1/pubpaa/US08 NEW PUB.pep.*
- 5: /SIDSS/ptodata/1/pubpaa/PCT_NEW PUB.pep.*
- 6: /SIDSS/ptodata/1/pubpaa/US09 NEW PUB.pep.*
- 7: /SIDSS/ptodata/1/pubpaa/US09 NEW PUB.pep.*
- 8: /SIDSS/ptodata/1/pubpaa/US10 NEW PUB.pep.*
- 9: /SIDSS/ptodata/1/pubpaa/US10 NEW PUB.pep.*
- 10: /SIDSS/ptodata/1/pubpaa/US11 NEW PUB.pep.*
- 11: /SIDSS/ptodata/1/pubpaa/US11 NEW PUB.pep.*
- 12: /SIDSS/ptodata/1/pubpaa/US10 NEW PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2131	100.0	397	11	US-11-253-151-33
2	577.5	27.1	444	11	US-11-253-151-33
3	574.5	27.0	464	9	US-10-745-586-112
4	505.5	23.7	468	11	US-11-253-151-35
5	490.2	23.0	431	11	US-11-253-151-32
6	371.7	17.4	273	11	US-11-253-151-8
7	364.5	17.1	258	11	US-11-253-151-9
8	132	6.2	4544	9	US-10-501-035-214
9	132	6.2	4544	11	US-11-076-427A-32
10	123	5.8	1170	11	US-11-114-962-5
11	118.5	5.6	2556	11	US-11-050-346-67
12	114.5	5.4	1433	11	US-11-114-962-1
13	110	5.2	971	8	US-10-505-928-397
14	108.5	5.1	1268	9	US-10-453-372-1144
15	108.5	5.1	1268	9	US-10-453-372-1154
16	108.5	5.1	1288	9	US-10-453-372-1146
17	108.5	5.1	1288	9	US-10-453-372-1152
18	108	5.1	1400	9	US-10-821-234-1045
19	106	5.0	2911	11	US-11-050-617-706
20	105.5	5.0	401	11	US-11-072-175-224
21	104	4.9	1193	11	US-11-022-478-8

22	103	4.8	1379	11	US-11-114-962-4	Sequence 4, Appl
23	102	4.8	999	11	US-11-113-424-36	Sequence 36, Appl
24	102	4.8	1067	11	US-11-209-137-3	Sequence 3, Appl
25	102	4.8	1067	11	US-11-054-912-3	Sequence 3, Appl
26	102	4.8	1218	9	US-10-501-035-303	Sequence 303, App
27	102	4.8	1218	11	US-11-078-735-20	Sequence 20, Appl
28	102	4.8	1218	11	US-11-050-346-65	Sequence 65, Appl
29	102	4.8	1218	11	US-11-103-077-20	Sequence 20, Appl
30	102	4.8	1218	11	US-11-072-175-155	Sequence 155, App
31	102	4.8	1218	11	US-11-022-478-4	Sequence 4, Appl
32	102	4.8	1218	11	US-11-209-137-1	Sequence 1, Appl
33	102	4.8	1218	11	US-11-054-912-1	Sequence 1, Appl
34	102	4.8	1218	11	US-11-058-066-20	Sequence 20, Appl
35	101	4.7	997	11	US-11-080-991-50	Sequence 50, Appl
36	100	4.7	728	11	US-11-022-478-11	Sequence 11, Appl
37	100	4.7	969	9	US-10-055-877-214	Sequence 214, App
38	100	4.7	1620	9	US-10-453-372-868	Sequence 868, App
39	99.5	4.7	712	11	US-11-050-857-952	Sequence 952, App
40	99.5	4.7	806	11	US-11-050-857-951	Sequence 951, App
41	99.5	4.7	970	11	US-11-050-857-950	Sequence 950, App
42	99.5	4.7	1083	11	US-11-050-857-949	Sequence 949, App
43	99.5	4.7	1292	11	US-11-050-857-948	Sequence 948, App
44	99.5	4.7	1346	11	US-11-050-857-947	Sequence 947, App
45	99.5	4.7	1419	11	US-11-114-962-3	Sequence 3, Appl

ALIGNMENTS

RESULT 1

US-11-253-151-33
; Sequence 33, Application US/11253151
; Publication No. US2006069242A1
; GENERAL INFORMATION:
; APPLICANT: MASURE, STEFAN L.J.
; APPLICANT: CIR, MIROSLAV
; APPLICANT: HOEFNAGEL, EVERT W.
; TITLE OF INVENTION: NEUROTROPIC FACTOR RECEPTOR
; FILE REFERENCE: JAB-1512
; CURRENT APPLICATION NUMBER: US/11/253,151
; PRIOR FILING DATE: 2005-10-18
; PRIOR APPLICATION NUMBER: PCT/EP00/04918
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 9915200.1
; PRIOR FILING DATE: 1999-06-29
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 33
; LENGTH: 397
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-253-151-33

Query Match	100.0%	Score	2131	DB	11	Length	397
Best Local Similarity	100.0%	Pred. No.	1.1e-191				
Matches	397	Conservative	0	Mismatches	0	Indels	0
Gaps	0						
Qy	1	MGLSWSPRPPLMLLLVLSLPLGAGNSLATENFVNSCTOARKKCEANPACKAAAYQH	60				
Db	1	MGLSWSPRPPLMLLLVLSLPLGAGNSLATENFVNSCTOARKKCEANPACKAAAYQH	60				
Qy	61	LGSCTSLSRPLPLEESAMSDCLEAAEQRLNSLIDCRHRRMKHOATCLDIYTWVHPA	120				
Db	61	LGSCTSLSRPLPLEESAMSDCLEAAEQRLNSLIDCRHRRMKHOATCLDIYTWVHPA	120				
Qy	121	RSIGDYELDVSPYEDVTVTSKPWONTSKLNMKPDSDCLKPFAMLTCLDHPKCDRLRKAYG	180				
Db	121	RSIGDYELDVSPYEDVTVTSKPWONTSKLNMKPDSDCLKPFAMLTCLDHPKCDRLRKAYG	180				
Qy	181	EACSGIRCQRHLCIAQLRSFFFEKAASHAQGLILCCAPEDAGCGRRRTTIAPSCALPS	240				
Db	181	EACSGIRCQRHLCIAQLRSFFFEKAASHAQGLILCCAPEDAGCGRRRTTIAPSCALPS	240				

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QY 241 VTNCNLDLRSFCRADPCLRSRLMDFTQCHPMDILGTCAEQSRCLRAYLGLIGTAMTN 300
Db 241 VTNCNLDLRSFCRADPCLRSRLMDFTQCHPMDILGTCAEQSRCLRAYLGLIGTAMTN 300
QY 301 FISKVNTTVALSCTCRGSGNLQDECEQLERSFSQNPCLVEATAAKMRPHQLFSQDWADS 360
Db 301 FISKVNTTVALSCTCRGSGNLQDECEQLERSFSQNPCLVEATAAKMRPHQLFSQDWADS 360
QY 361 TFSVVOQNSNPALRQPRLPILSFLPILLOTLW 397
Db 361 TFSVVOQNSNPALRQPRLPILSFLPILLOTLW 397
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RESULT 2

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US-11-253-151-34
; Sequence 34, Application US/11253151
; Publication No. US20060069242A1
```

GENERAL INFORMATION:

```
; APPLICANT: MASURE, STEFAN L.J.
; APPLICANT: CIK, MIROSLAV
; APPLICANT: HOEFNAGEL, EVERT W.
; TITLE OF INVENTION: NEUROTROPHIC FACTOR RECEPTOR
; FILE REFERENCE: JAB-1512
; CURRENT APPLICATION NUMBER: US/11/253,151
; PRIOR FILING DATE: 2005-10-18
; PRIOR APPLICATION NUMBER: PCT/EP00/04918
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 9915200.1
; PRIOR FILING DATE: 1999-06-29
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: Patentin Ver. 3.2
; SEQ ID NO 34
; LENGTH: 444
; TYPE: PRT
; ORGANISM: Rattus rattus
; US-11-253-151-34
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Query Match 27.1%; Score 577.5; DB 11; Length 444;

Best Local Similarity 38.8%; Pred. No. 3.7e-46; Mismatches 125; Indels 35; Gaps 9;

Matches 127; Conservative 40; Mismatches 125; Indels 35; Gaps 9;

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QY 41 CTQARKKEANPACKAAAYQHLGSCSTSSLSRPLPLEESAMSADCLEAAEQLRNSSLDCRC 100
Db 40 CVRANELCAAESNCSSRYTLRQCLAGRDNTML-----ANKEQAALEVLQESPLYDCRC 95
QY 101 HRMKHQATCLDIYVTVHPARSLGDYELDVSPYEDVTTSKPMKMLSKLML-----152
Db 96 KRGMKELQCLQIYWSIHLGLTEGEFYEASPYE-PVTSR-----LSDIFRLASIFSGTG 149
QY 153 -----KPDSDLCLKPFAMLCITLHDKCDRLRKAYGEACS-----GIRCORHLCLAQLRSFPE 202
Db 150 TDPAVTSKSNHCLDAKACNLNDNCKLRSSYISICNREISPTERCNRKCHKALRQFFD 209
QY 203 KAAESHAQGLLCPACEDAGGERRNTIAPSCAL-PSVTPNCLDLRSFCRADPCLCRSR 261
Db 210 RVSEYTYRMLFSC--QDQACAEERRQTILPSCSYEDKEKPNCLDLRSICRTDHLCRSR 267
QY 262 LMDFTQCHP--MDILGTCAEQSRCLRAYLGLIGTAMTNPFIKSVNTTVALS--CTCRG 317
Db 268 LADFHANCASRYTITSCPADNYQACLGSYAGMIGFDMTPNYVDSSPTGIVVSPWCNCRG 327
QY 318 SGNLQDECEQLERSFSQNPCLVEATAIA 344
Db 328 SGNMEECEKFLRDFTEPNCLRNAIQ 354
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RESULT 3

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US-10-745-586-112
; Sequence 112, Application US/10745586
; Publication No. US20060063227A1
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GENERAL INFORMATION:

```
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John M.
```

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; APPLICANT: LaVallie, Edward R.
; APPLICANT: Collins-Racie, Lisa A.
; APPLICANT: Evans, Cheryl
; APPLICANT: Merberg, David
; APPLICANT: Treacy, Maurice
; APPLICANT: Bowman, Michael R.
; APPLICANT: Spaulding, Vikki
; APPLICANT: Agostino, Michael J.
; APPLICANT: Genetics Institute, Inc.
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
; FILE REFERENCE: GI 6011-18X
; CURRENT APPLICATION NUMBER: US/10/745,586
; PRIOR FILING DATE: 2003-12-29
; PRIOR APPLICATION NUMBER: US/09/398,829
; PRIOR FILING DATE: 1999-09-17
; NUMBER OF SEQ ID NOS: 283
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 112
; LENGTH: 464
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-745-586-112
```

Query Match 27.0%; Score 574.5; DB 9; Length 464;

Best Local Similarity 37.9%; Pred. No. 7.5e-46;

Matches 124; Conservative 44; Mismatches 124; Indels 35; Gaps 9;

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QY 41 CTQARKKEANPACKAAAYQHLGSCSTSSLSRPLPLEESAMSADCLEAAEQLRNSSLDCRC 100
Db 40 CVRANELCAAESNCSSRYTLRQCLAGRDNTML-----ANKEQAALEVLQESPLYDCRC 95
QY 101 HRMKHQATCLDIYVTVHPARSLGDYELDVSPYEDVTTSKPMKMLSKL-----149
Db 96 KRGMKELQCLQIYWSIHLGLTEGEFYEASPYE-PVTSR-----LSDIFRLASIFSGTG 149
QY 150 --NMLKPDSDLCLKPFAMLCITLHDKCDRLRKAYGEACS-----GIRCORHLCLAQLRSFPE 202
Db 150 ADPVVSAXSNHCLDAKACNLNDNCKLRSSYISICNREISPTERCNRKCHKALRQFFD 209
QY 203 KAAESHAQGLLCPACEDAGGERRNTIAPSCAL-PSVTPNCLDLRSFCRADPCLCRSR 261
Db 210 RVSEYTYRMLFSC--QDQACAEERRQTILPSCSYEDKEKPNCLDLRGVCTDHLCRSR 267
QY 262 LMDFTQCHP--MDILGTCAEQSRCLRAYLGLIGTAMTNPFIKSVNTTVALS--CTCRG 317
Db 268 LADFHANCASRYTITSCPADNYQACLGSYAGMIGFDMTPNYVDSSPTGIVVSPWCNCRG 327
QY 318 SGNLQDECEQLERSFSQNPCLVEATAIA 344
Db 328 SGNMEECEKFLRDFTEPNCLRNAIQ 354
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RESULT 4

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US-11-253-151-35
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; Sequence 35, Application US/11253151
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; Publication No. US20060069242A1
```

GENERAL INFORMATION:

```
; APPLICANT: MASURE, STEFAN L.J.
; APPLICANT: CIK, MIROSLAV
; APPLICANT: HOEFNAGEL, EVERT W.
; TITLE OF INVENTION: NEUROTROPHIC FACTOR RECEPTOR
; FILE REFERENCE: JAB-1512
; CURRENT APPLICATION NUMBER: US/11/253,151
; CURRENT FILING DATE: 2005-10-18
; PRIOR APPLICATION NUMBER: PCT/EP00/04918
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 9915200.1
; PRIOR FILING DATE: 1999-06-29
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: Patentin Ver. 3.2
; SEQ ID NO 35
; LENGTH: 468
; TYPE: PRT
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; ORGANISM: Rattus rattus
US-11-253-151-35

Query Match      23.7%; Score 505.5; DB 11; Length 468;
Best Local Similarity 35.6%; Pred. No. 2.2e-39;
Matches 127; Conservative 40; Mismatches 145; Indels 45; Gaps 13;

Qy 10 PLMLILLVLSLWPLGAGNSLATENRFVNSCTQARKKCEANPACKAAAYQHILGSCSTSL 69
Db 11 PLDLLMSA-----EVSGGRL-----DCVKASDQCLKEQSCSTKYRTLRLQCVA 57

Qy 70 RPLPLESAMSAD-CLEAAQLRNSLIDCRCHRMKHQATCLDIYVTHVHARS-LGDYE 127
Db 58 TNFSLTSGLEAKDECRSAMBALKOKLYNCRCKRGKKCKNCLRIYWSMY--OSLQGN 115

Qy 128 LDVSPYEDTVTSKPKWNLKSLKMLKP-DSDL-----CLKFAMLCITLHDKKDR 174
Db 116 LEDSPYE-----PVNSRLSDIFRAVPFFISDVQQVEHISKGNCLDAKACNLDTC 169

Qy 175 LRKAYGEAC-----SGIRCORHLCLAQRLRSFFKAAESHAQGLLLCPCAPEDAGC 230
Db 170 YRSAYITPCTTMSNEVNRKCKHALRQFFDKVPKHSYGMVLCFCSC--RDIACTERR 227

Qy 231 TIAPSCALPS-VTPNCLDLRSFCRADPLCRSLRMLDPQTHCPMD-ILGTCAEQ-SRCL 287
Db 228 TIIVPVCSEYERPNCLSLQDSCKTWYICRSRLADFTTNCOPESRSVSNCLKENYAD 287

Qy 288 AYVGLIGTAMTPNFISKVNTTVALSCTCRSGNLODECEQLERSFSONPCLVEATAA 344
Db 288 AYSGLIGTWTNPNYDVSSLSVAPWPCDSCNSGNDLEDCLKFLNFQDNTCLKNAIQA 344

RESULT 5
US-11-253-151-32
; Sequence 32, Application US/11253151
; Publication No. US20060069242A1
; GENERAL INFORMATION:
; APPLICANT: MASURE, STEFAN L.J.
; APPLICANT: CIK, MIROSLAV
; APPLICANT: HOEFNAGEL, EVERT W.
; TITLE OF INVENTION: NEUROTROPHIC FACTOR RECEPTOR
; FILE REFERENCE: JAB-1512
; CURRENT APPLICATION NUMBER: US/11/253,151
; PRIOR FILING DATE: 2005-10-18
; PRIOR FILING DATE: 2000-05-26
; PRIOR FILING DATE: 2000-05-26
; PRIOR FILING DATE: 1999-06-29
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 32
; LENGTH: 431
; TYPE: PRT
; ORGANISM: Gallus gallus
US-11-253-151-32

Query Match      23.0%; Score 490; DB 11; Length 431;
Best Local Similarity 32.8%; Pred. No. 5.6e-38;
Matches 120; Conservative 50; Mismatches 158; Indels 38; Gaps 12;

Qy 41 CTQARKKEANPACKAAAYQHILGSCSTSLRPLPLEBSAMSDCLAEAAQLRNSLIDCRC 100
Db 26 CLQAGESBCTNPICSSKFRTRLCIAG-NGANKLGPDAXN-QCRSTVTALLSSQLYGCK 83

Qy 101 HRRMKHQATCLDIYVTHVHARSIGDYELDVSPYEDTVTSKPKWNLKSLKMLKPDS- 157
Db 84 KRGMKKKCKHCLSVYSHIHTLEGMNVLESSEYPPIRG-----FDYVRLASITAGSE 139

Qy 158 -----LCIKPAMLCITLHDKDRLKAYGEACSGIR-----CORHLCLAQRLRSFF 206
Db 140 TQVNRCLDAKACNVDEMQRLETVTSFC--IRRLARADTCNRKCHKALKRKFDRVPP 197

Qy 207 SHAQGLLLCPCAPEDAGCGERRRNTIAPSCALPS-VTPNCLDLRSFCRADPLCRSLMD 265

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Db 2940 HINECLSRKLSG-----CSQDCD 2958

RESULT 10

US-11-114-962-5

Sequence 5, Application US/11114962

Publication No. US20060030694A1

GENERAL INFORMATION:

APPLICANT: Kitajewski, Jan

APPLICANT: Shawber, Carrie

APPLICANT: Funahashi, Yasuhiro

TITLE OF INVENTION: Notch-Based Fusion Proteins And Uses Thereof

FILE REFERENCE: 0575/71308-A

CURRENT APPLICATION NUMBER: US/11/114,962

CURRENT FILING DATE: 2005-04-26

NUMBER OF SEQ ID NOS: 14

SOFTWARE: PatentIn version 3.3

SEQ ID NO 5

LENGTH: 1170

TYPE: PRT

ORGANISM: Mus musculus

US-11-114-962-5

Query Match 5.8%; Score 123; DB 11; Length 1170;

Best Local Similarity 22.6%; Pred. No. 0.0044;

Matches 81; Conservative 33; Mismatches 156; Indels 88; Gaps 19;

QY 40 SCTQARKKCEANP-----ACKAAVQHLG-SCTSSLSRPLPLEESAMSADCL 84

Db 722 TCSEEVACHSGCLNGSGCSIRPEGYSCTCLPSHTGRHCQTAV-----DHCVSASCL 774

QY 85 EA-----AEQLRNSLLDCRCHRRMKHOATCLDIYVTHVPARS 122

Db 775 NGGTCVKNKPTFFCLCATGQGLHCEBETNPSCADSPC-----RNKATCQD---TPRGARC 827

QY 123 L---GDYELDVSPVEDVTTSKPWONLSKMLKPDSDLCLK--FAMLC TLHDKCDRLRK 177

Db 828 LCSPGYTGSSCQTILDLCAKPCPHTARCLQSGPSFQCLCLQGTGALCDFPLSCQKAA 887

QY 178 AYEACSGIRCOR-HLCLAQLRSFEKAAESHAQGLL---LCPCADGACGGERNTI 232

Db 888 SQGIBISGL-CQNGGLCIDTGSYSYFCRPPGF-QGKLQDNVNPCEPNCHHG---STC 941

QY 233 AP-----SCALPSVTPNCLDLRSFCRADP-----LCRSLRMDLQFCHHPMDILGTCA 280

Db 942 VPQSGYVQCAGPYEQNSKVLDAQSQPCNHNHGTCTSRPGGFHCACPPGFVGLRCBG 1001

QY 281 EQSRCLRAYLGLIGTAMTPNFISKVNTVALSCTCRGSGNLQDECEQLRSFSQNP-PC 337

Db 1002 DVDECLDRPCHPSGTAACHSLAN-----AFYCQCL-PGHTGQRCB-VENDLQSQSPC 1051

RESULT 11

US-11-050-346-67

Sequence 67, Application US/11050346

Publication No. US20060002924A1

GENERAL INFORMATION:

APPLICANT: BODMER, MARK WILLIAM

APPLICANT: CHAMPION, BRIAN ROBERT

APPLICANT: LENNARD, ANDREW CHRISTOPHER

APPLICANT: MCKENZIE, GRAHAME JAMES

APPLICANT: TUGAL, TAMARA

APPLICANT: WARD, GEORGE ALBERT

TITLE OF INVENTION: CONJUGATE OF NOTCH SIGNALLING PATHWAY MODULATORS AND THEIR USE IN MEDICAL TREATMENT

FILE REFERENCE: 674525-2016

CURRENT APPLICATION NUMBER: US/11/050,346

CURRENT FILING DATE: 2005-02-03

PRIOR APPLICATION NUMBER: GB 0312062.3

PRIOR FILING DATE: 2003-05-24

PRIOR APPLICATION NUMBER: PCT/GB03/01525

PRIOR FILING DATE: 2003-04-04

QY 39 NSTQARKKCEANPCKAAVQHLGSGTSSLSRPL-----PLEESAMSAD-CLAEAAQLRNS 94

Db 379 NPCNEG-SNCDTNPVNGKA---ICTCPSGYTGACQDVDECSLGANPCBHGAKCINTLG 434

QY 95 LIIDCRC-----HRRMKHOATCLDIYVTHVPARSIGDYELDVSP-YE-- 134

Db 435 SFCQCLQGYTGPRCIDVNECVSNPCNDATCLD-----QIGFQCMCPGYEGY 485

QY 135 -----DITVTSKPKWN---LSKLN-----MLKPDSDLCLK----- 161

Db 486 HCEVNTDECASSPCLHNGRCLDKINEFQCECPGFTGHLCOYDVDECASTPCNKGAKCLD 545

QY 162 -----FAMLC T-----LH-----DKDRLRAYGEACSGIRCORHLCLAQLRSFEKAAES 207

Db 546 GPNTYTCVCTEGYTGTHCEVDIDECDFDPCHYSGCKDGVATFTCLCRP---GYTGHHCET 602

QY 208 HAQGLLLCPCA-----PEDACGGERRNTIAPSCAL-----PSVTPNCLD-LRSF 251

Db 603 NINECSSQPCRLRGTCQDPDNAYLCFLKGTGTGPNCEINLDDCASSPCDSTCLDKIDGY 662

QY 252 -CRADP-----LCRSLRMDLQFTH-CHPMDILGTCAFE---QSRCLRAYLGLIGTAMTPN 300

Db 663 ECACEFGYTGSMNSNIDECAGNPCHNG---GICEGNGFTCRCEGY-----HDPT 712

QY 301 FISKVNTVALSC---TCRSGN-----LQDECEQLRSFSQNPCL 338

Db 713 CLSEVNECNSPCVHCACRDSLNGYKCDPCGWSGTGNTCDINNNECE-----SNPCV 763

RESULT 12

US-11-114-962-1

Sequence 1, Application US/11114962

Publication No. US20060030694A1

GENERAL INFORMATION:

APPLICANT: Kitajewski, Jan

APPLICANT: Shawber, Carrie

APPLICANT: Funahashi, Yasuhiro

TITLE OF INVENTION: Notch-Based Fusion Proteins And Uses Thereof

FILE REFERENCE: 0575/71308-A

CURRENT APPLICATION NUMBER: US/11/114,962

CURRENT FILING DATE: 2005-04-26

NUMBER OF SEQ ID NOS: 14

SOFTWARE: PatentIn version 3.3

QY 39 NSTQARKKCEANPCKAAVQHLGSGTSSLSRPL-----PLEESAMSAD-CLAEAAQLRNS 94

Db 379 NPCNEG-SNCDTNPVNGKA---ICTCPSGYTGACQDVDECSLGANPCBHGAKCINTLG 434

QY 95 LIIDCRC-----HRRMKHOATCLDIYVTHVPARSIGDYELDVSP-YE-- 134

Db 435 SFCQCLQGYTGPRCIDVNECVSNPCNDATCLD-----QIGFQCMCPGYEGY 485

QY 135 -----DITVTSKPKWN---LSKLN-----MLKPDSDLCLK----- 161

Db 486 HCEVNTDECASSPCLHNGRCLDKINEFQCECPGFTGHLCOYDVDECASTPCNKGAKCLD 545

QY 162 -----FAMLC T-----LH-----DKDRLRAYGEACSGIRCORHLCLAQLRSFEKAAES 207

Db 546 GPNTYTCVCTEGYTGTHCEVDIDECDFDPCHYSGCKDGVATFTCLCRP---GYTGHHCET 602

QY 208 HAQGLLLCPCA-----PEDACGGERRNTIAPSCAL-----PSVTPNCLD-LRSF 251

Db 603 NINECSSQPCRLRGTCQDPDNAYLCFLKGTGTGPNCEINLDDCASSPCDSTCLDKIDGY 662

QY 252 -CRADP-----LCRSLRMDLQFTH-CHPMDILGTCAFE---QSRCLRAYLGLIGTAMTPN 300

Db 663 ECACEFGYTGSMNSNIDECAGNPCHNG---GICEGNGFTCRCEGY-----HDPT 712

QY 301 FISKVNTVALSC---TCRSGN-----LQDECEQLRSFSQNPCL 338

Db 713 CLSEVNECNSPCVHCACRDSLNGYKCDPCGWSGTGNTCDINNNECE-----SNPCV 763

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; SEQ ID NO 1
; LENGTH: 1433
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-11-114-962-1

Query Match      5.4%; Score 114.5; DB 11; Length 1433;
Best Local Similarity 19.9%; Pred. No. 0.035;
Matches 85; Conservative 40; Mismatches 132; Indels 171; Gaps 26;

QY 39 NSCTOARKKEANPA-----CKAAYQHLAGSCTSSLSRPLPLFSAMSAD-CLEAARQLRN 92
DB 379 NPCNEG-SNCDTPVNGKAICTCPRGVGTGACQ-----DVDESCALGANPCEHAGKCLNT 432
QY 93 SSLIDCRC-----HRRMKHQATCLDIYVTHVPARSLSGDYELDVSP-YE 134
DB 433 LGSFEQCQCLQGYTGPRCEIDVNECISNPQNDAATCLD-----QIGEFQICMPGYE 483
QY 135 -----DVTGSKPMKN--LKLNL-----MLKPDSDLCLK----- 161
DB 484 GVTCEINTDECASPCLNHRCVDKINEFLCQPKGFSGHLCOYDVDECASTPCKNGAKC 543
QY 162 -----FAMLC-----LH-----DKCDRLRKAYGEACSGIR-----CQ-----RHLCIAQ 196
DB 544 LDGPNYTCVCTEGYTGTHCEVDIDECDDPPCHIGLCKDGVATFTCLCQPGVYTGHCETN 603
QY 197 LRSFFEKAESHAQGLLLCPCAPEDAGCGERRNTIAPSCALPSVTPNCLDLRSFCRADP 256
DB 604 IN-----ECHSQ-----PC--RHGGTCQDRDNYLYLCLKGTGTPNCEINLDDCASNP 649
QY 257 -----LCRSRLMDFTQCHP-----MDIL-----GTC-----ATEQSRCLRAYL 290
DB 650 CDSGTCLDKIDGECACEPEGYTGSMCNVNDICAGSPCHNGGTCEDGIAGFTCRCEGY- 708
QY 291 GLIGTATPNFISKVNTTVALSC---TCRGSNG-----LQDECEQLER 330
DB 709 -----HDPTCLSEVNECNSPCIHGACRDGLNGKDCAPGWSGTNCDINNNECE---- 758
QY 331 SFSQNPCL 338
DB 759 ---SNPCV 763

RESULT 13
US-10-505-928-397
; Sequence 397, Application US/10505928
; Publication No. US2006089532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; PRIOR FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2
; SEQ ID NO 397
; LENGTH: 971
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-505-928-397

Query Match      5.2%; Score 110; DB 8; Length 971;
Best Local Similarity 19.7%; Pred. No. 0.057;
Matches 100; Conservative 168; Mismatches 168; Indels 182; Gaps 26;

QY 22 WLPPLGAGN-SLATENRFVNSCTOARKKEANPACKAAYOH-LGSCTS----- 66
DB 99 WVGLGOCCELAIALECR--QACKQASSKNDISKVCKEYENALFSCISRNEMGVCCSYAG 156
QY 67 -----SLSRPLPLEBSAMSADCLEAAEQ-----RN--SSLID 97

; SEQ ID NO 144
; LENGTH: 1268
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-453-372-1144

Query Match      5.1%; Score 108.5; DB 9; Length 1268;
Best Local Similarity 21.1%; Pred. No. 0.11;
Matches 85; Conservative 34; Mismatches 159; Indels 125; Gaps 21;
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QY 25 LGAGNSLATENRFVNSCTQARK--KCEAN-----PACKAAYQHLGSCSTSSLSRPLPLE-- 75
Db 272 LGGSCVDLVGNVTCLCAEPFKGLRCBTGDHPVPDACLAPCHNGGTCVDADQGVCECP 331
QY 76 ESAMSDACLEAAEQLRNSSLIDCECHRMKHQATCLDIYWTVHPARSLGDYELDVSPYED 135
Db 332 EGFMLDCRERVDP-----DCEC-----RNGRCLGANTTLCQC-PLGFFGL-LCBFE- 377
QY 136 TVTSKPKWMLSKLNMKLPDSDLCKF--AMLCTLH-----DKC 172
Db 378 -ITAMPNMNTQ-----CPDGGYCMHGGSYLVCVCHTDHNASHSLSLPSDCSDPCFNGGSC 431
QY 173 DRLRKAYGEAC-----SGIRCOR---HLCLA-----QLRSFPEKAAESHAQ----- 210
Db 432 DAHDDSYTCPCPRGFHGKHKCEKARPHLCSSGPCRNGGTCKEAGGEYHCSCPFRFTGRHCE 491
QY 211 -----GULLCPCAPEDAGCGERRNTTAPS-CALPSVTTPNCLD 247
Db 492 IGKPDSCASGFCNNGGTCFHYIGKYKDCPPGFSG-----RHCEIAPSPC----- 536
QY 248 LRSFCRADPLCRSLRMDFQTHCHPMDILGTCAE-----QSRCLRAYLGLIGTAMTNPFI 302
Db 537 FRSPCVNGGTCEDRDTDFCHCQAGYMGRCQAEVDCGPPPEVKHATLRFNGTFLGVAL 596
QY 303 SKYNTTVALS-----CTCRGSGNLQDECEQLERSFSQNPCL 338
Db 597 YACDRGYSLAPSRIKRVCPHGVWSEPPQCLEIDECRSQ-PCL 638

RESULT 15
US-10-453-372-1154
; Sequence 1154, Application US/10453372
; Publication No. US2006003232A1
; GENERAL INFORMATION:
; APPLICANT: Alsbrook, et al.
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-589 A
; CURRENT APPLICATION NUMBER: US/10/453,372
; CURRENT FILING DATE: 2003-06-03
; PRIOR APPLICATION NUMBER: 09/789390
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/185967
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 09/823187
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/195792
; PRIOR FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: 09/839446
; PRIOR FILING DATE: 2001-03-19
; PRIOR APPLICATION NUMBER: 60/199476
; PRIOR FILING DATE: 2000-03-25
; PRIOR APPLICATION NUMBER: 09/863776
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 60/208263
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: 09/939398
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 60/227800
; PRIOR FILING DATE: 2000-08-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1609
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 1154
; LENGTH: 1268
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-453-372-1154
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Query Match 5.1%; Score 108.5; DB 9; Length 1268;
Best Local Similarity 21.1%; Pred. No. 0.11;
Matches 85; Conservative 34; Mismatches 159; Indels 125; Gaps 21;

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QY 25 LGAGNSLATENRFVNSCTQARK--KCEAN-----PACKAAYQHLGSCSTSSLSRPLPLE-- 75
Db 272 LGGSCVDLVGNVTCLCAEPFKGLRCBTGDHPVPDACLAPCHNGGTCVDADQGVCECP 331
QY 76 ESAMSDACLEAAEQLRNSSLIDCECHRMKHQATCLDIYWTVHPARSLGDYELDVSPYED 135
Db 332 EGFMLDCRERVDP-----DCEC-----RNGRCLGANTTLCQC-PLGFFGL-LCBFE- 377
QY 136 TVTSKPKWMLSKLNMKLPDSDLCKF--AMLCTLH-----DKC 172
Db 378 -ITAMPNMNTQ-----CPDGGYCMHGGSYLVCVCHTDHNASHSLSLPSDCSDPCFNGGSC 431
QY 173 DRLRKAYGEAC-----SGIRCOR---HLCLA-----QLRSFPEKAAESHAQ----- 210
Db 432 DAHDDSYTCPCPRGFHGKHKCEKARPHLCSSGPCRNGGTCKEAGGEYHCSCPFRFTGRHCE 491
QY 211 -----GULLCPCAPEDAGCGERRNTTAPS-CALPSVTTPNCLD 247
Db 492 IGKPDSCASGFCNNGGTCFHYIGKYKDCPPGFSG-----RHCEIAPSPC----- 536
QY 248 LRSFCRADPLCRSLRMDFQTHCHPMDILGTCAE-----QSRCLRAYLGLIGTAMTNPFI 302
Db 537 FRSPCVNGGTCEDRDTDFCHCQAGYMGRCQAEVDCGPPPEVKHATLRFNGTFLGVAL 596
QY 303 SKYNTTVALS-----CTCRGSGNLQDECEQLERSFSQNPCL 338
Db 597 YACDRGYSLAPSRIKRVCPHGVWSEPPQCLEIDECRSQ-PCL 638
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Search completed: May 12, 2006, 02:16:16
Job time : 20.4266 secs

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Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	1646.5	75.2	397	2	JE0082	GPI-linked receptor
2	147	6.7	2703	1	A24420	notch protein - fr
3	133.5	6.1	3084	1	MMWSA	laminin alpha-1 ch
4	124	5.7	1700	2	S08167	Balbani ring 3 pr
5	123.5	5.6	2195	2	S34264	hypothetical prote
6	123.5	5.6	2871	2	A35567	fibillin I - bovi
7	123.5	5.6	3002	2	A47221	fibillin-1 precu
8	120	5.5	1964	2	T09059	notch4 - mouse
9	117.5	5.4	2704	2	S01118	G surface protein
10	116	5.3	3635	2	T10053	laminin alpha 5 ch
11	115	5.3	2531	2	A48019	notch-1 protein -
12	115	5.3	5376	2	T42215	zonadhesin - mouse
13	114.5	5.2	1106	2	T44598	hypothetical prote
14	114.5	5.2	2871	2	A55624	fibillin-1 precu
15	114	5.2	1034	2	JC5598	mucin - rat
16	114	5.2	2531	2	S18188	notch protein homo
17	112.5	5.1	2555	2	A40043	notch protein homo
18	112.5	5.1	4543	1	A53102	alpha-2-macroglobu
19	111.5	5.1	1106	2	T19338	gene shuttle craft
20	111.5	5.1	1609	1	MMHUB2	laminin gamma-1 ch
21	110	5.0	2321	2	S78549	notch3 protein - h
22	110	5.0	4544	1	S02392	alpha-2-macroglobu
23	109.5	5.0	949	2	T24294	hypothetical prote
24	109	5.0	2139	2	A35672	crumbs protein - f
25	108.5	5.0	4545	1	S23111	alpha-2-macroglobu
26	108	4.9	2718	2	A34715	G surface protein
27	106	4.8	473	2	A56175	adhesive plaque pr
28	106	4.8	2918	2	A54105	fibillin-2 precu
29	105	4.8	593	2	A54281	coagulation factor

A;Reference number: S02678; MUID:89326259; PMID:2458101
A;Accession: S02678
A;Molecule type: protein
A;Residues: 630-642.'D'.644:2690-2704 <EU3>
A;Cross-references: UNIPARC:UPI0000173CA4; UNIPARC:UPI0000173CAE
R;Deutzmann, R.; Huber, J.; Schmets, K.A.; Oberbaumer, I.; Hartl, L.
Eur. J. Biochem. 177, 35-45, 1988
A;Title: Structural study of long arm fragments of laminin. Evidence for repetitive C-
A;Reference number: S01790; MUID:89030693; PMID:3181157
A;Accession: S01790
A;Molecule type: mRNA
A;Residues: 2538-3084 <DEU>
A;Cross-references: UNIPARC:UPI000016CE8E; EMBL:X13459; NID:955499; PIDN:CAA31807.1; PID
A;Accession: A30451
A;Molecule type: protein
A;Residues: 1911-1929;1997-2006;2033-2045.'X'.2047-2054.'X'.2056-2066.'X'.2068-2105;2120
470:2487-2498;2502-2525;2538-2557;2561-2591.'X'.2593-2594;2600-2610;2616-2645;2648-2655;
93:2998-3005.'A'.3007-3033.'V'.3035;3068-3083 <DE2>
A;Cross-references: UNIPARC:UPI0000173CB6; UNIPARC:UPI0000173CB7; UNIPARC:UPI0000173CB8;
CBD; UNIPARC:UPI0000173CBE; UNIPARC:UPI0000173CBF; UNIPARC:UPI0000173CC0; UNIPARC:UPI000
1000173CC6; UNIPARC:UPI0000173CC7; UNIPARC:UPI0000173CC8; UNIPARC:UPI0000173CC9; UNIPAR
A;Note: 2256-Val was also found
R;Olson, D.; Nagayoshi, T.; Pazio, M.; Peltonen, J.; Jaakkola, S.; Sanborn, D.; Sasaki,
Lab. Invest. 60, 772-782, 1989
A;Title: Human laminin: cloning and sequence analysis of cDNAs encoding A, B1 and B2 cha
A;Reference number: A34961; MUID:89280632; PMID:2733383
A;Accession: S14670
A;Molecule type: protein
A;Residues: 2424-2436;2440-2451;2461-2467;2487-2525;2550-2557;2561-2593;2600-2610;2616-2
-2942.'T'.2944-2964;2969-2976;2980-2993;2998-3000.'I'.3002-3018.'V'.3020-3034;3068-3083
A;Cross-references: UNIPARC:UPI0000173C9E; UNIPARC:UPI0000173CAE; UNIPARC:UPI0000173CBC;
C7; UNIPARC:UPI0000173CC8; UNIPARC:UPI0000173CCA; UNIPARC:UPI0000173CCB; UNIPARC:UPI000
1000173CD1; UNIPARC:UPI0000173CD2; UNIPARC:UPI0000173CD3; UNIPARC:UPI0000173CD4; UNIPAR
C;Function: Laminins are trimers of an alpha-type, a beta-type, and a gamma-type laminin
A;Description: interact with cells and with other basement membrane proteins to promote
C;Superfamily: laminin alpha-1 chain; laminin G repeat homology; laminin-type EGF-like h
C;Keywords: basement membrane; calcium binding; cell binding; coiled coil; extracellular
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-3084/Product: laminin alpha-1 chain #status predicted <MAT>
F;25-277/Domain: VI <DOM6>
F;277-331/Domain: laminin-type EGF-like homology <LE01>
F;334-401/Domain: laminin-type EGF-like homology <LE02>
F;404-458/Domain: laminin-type EGF-like homology <LE03>
F;461-507/Domain: laminin-type EGF-like homology <LE04>
F;510-519/Domain: laminin-type EGF-like homology #status atypical <LE05>
F;520-715/Domain: IIV <DO4B>
F;716-1166/Domain: IIIB <DO3B>
F;716-746/Domain: laminin-type EGF-like homology #status atypical <LE06>
F;749-795/Domain: laminin-type EGF-like homology <LE07>
F;798-853/Domain: laminin-type EGF-like homology <LE08>
F;830-834/Region: cell adhesion #status predicted
F;856-906/Domain: laminin-type EGF-like homology <LE09>
F;909-955/Domain: laminin-type EGF-like homology <LE10>
F;958-1002/Domain: laminin-type EGF-like homology <LE11>
F;1005-1048/Domain: laminin-type EGF-like homology <LE12>
F;1051-1094/Domain: laminin-type EGF-like homology <LE13>
F;1097-1196/Domain: laminin-type EGF-like homology #status atypical <LE14>
F;1118-1154/Domain: laminin-type EGF-like homology #status atypical <LE15>
F;1147-1149/Region: cell attachment (R-G-D) motif
F;1157-1166/Domain: laminin-type EGF-like homology #status atypical <LE16>
F;1167-1368/Domain: IIV <DO4A>
F;1369-1561/Domain: IIIA <DO3A>
F;1369-1407/Domain: laminin-type EGF-like homology #status atypical <LE17>
F;1410-1456/Domain: laminin-type EGF-like homology <LE18>
F;1459-1513/Domain: laminin-type EGF-like homology <LE19>
F;1516-1560/Domain: laminin-type EGF-like homology <LE20>
F;1562-2133/Domain: II/I <DOM2>
F;1562-2133/Region: heptad repeats
F;2134-3084/Domain: G <DOMG>
F;2150-2308/Domain: laminin G repeat homology <LG1>
F;2337-2492/Domain: laminin G repeat homology <LG2>

F;2518-2683/Domain: laminin G repeat homology <LG3>
F;2748-2897/Domain: laminin G repeat homology <LG4>
F;2925-3082/Domain: laminin G repeat homology <LG5>
F;25/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted
F;45,79,370,374,331,562,672,808,914,959,969,1052,1344,1414,1586,1603,1659,1686,1706,171
e (Asn) (covalent) #status predicted
F;304-312/Diulfide bonds: #status experimental
F;770,857,1999,2055,2067,2835/Binding site: carbohydate (Asn) (covalent) #status exper
F;845,2102/Binding site: carbohydate (Asn) (covalent) #status absent

Query Match 6.1%; Score 133.5; DB 1; Length 3084;
Best Local Similarity 20.9%; Pred. No. 0.038;
Matches 78; Conservative 31; Mismatches 125; Indels 139; Gaps 21;
QY 50 KCQADPTCSAAVHHL--DSCTSSISTPLPEEESVPADCLEAAQQLR-NSLSIGCMCHRR 106
DB 757 ECDIHGICSVCTNTYTGDCHEQCQLPGFYGTFRGTGDCQPCACPLSIDNNFSPTCILT 816
QY 107 MKNQVA-----CLDIYW-----TVHRARSLGNVELDVSPYE-----DT 139
DB 817 DGEVVCDCQCAPGYSGSWCERCADGYGNPTVPGTVCPCNSGN-----VDPLEAGHCDS 872
QY 140 VTSKPKWNLKMLKPDSDILCLKFMCLTND---KCDRLKA-YGEACSGPHCQHV 195
DB 873 VTGE-----CLK-----CLMNTDGAHCERCADGFYGDVATKNC----- 906
QY 196 CLRQLLTFREKAAEPHAQGLL-----LCPCAPN-----DRGCGER 230
DB 907 -----RACDCHENGSLSGVCHLETGLCDCKPHVTVQQCDQCLSGYGLDTGLG-- 954
QY 231 RRNTIAPNCALP-FVAPNCLLELRRLCFSDPLCRSLRVDFQTH-----CHPMDILGT 280
DB 955 ---CVPNCSEVSGSDNCTE-EGQCHGPGVGKQCDRCRSHGFYAFQDGGCTPCD--- 1006
QY 281 CATEQSRCLRAYLGLGTAMTFNVNNTSV-----ALSCTRCSGNLQEE 327
DB 1007 CAHTQNNCDPA-----SGECLCPHTQGLKCEERAYWGLDPBQGCQACNCSAVGTSQA 1062
QY 328 CEMLEGFPSHNPC 340
DB 1063 CDVLSG---HCPC 1072

RESULT 4
S08167
Balbiani ring 3 protein - midge (Chironomus tentans)
C;Species: Chironomus tentans
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 16-Aug-2004
C;Accession: S08167
R;Paulsson, G.; Lendahl, U.; Gallii, J.; Ericsson, C.; Wieslander, L.
J. Mol. Biol. 211, 331-349, 1990
A;Title: The balbiani ring 3 gene in Chironomus tentans has a diverged repetitive struc
A;Reference number: S08167; MUID:90172404; PMID:1689777
A;Accession: S08167
A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-1700 <PAU>
A;Cross-references: UNIPROT:Q03376; UNIPARC:UPI0000126788; GB:X52263; NID:g7057; PIDN:C
C;Genetics:
A;Gene: BR3
A;Map position: 4
Query Match 5.7%; Score 124; DB 2; Length 1700;
Best Local Similarity 19.1%; Pred. No. 0.12;
Matches 89; Conservative 35; Mismatches 164; Indels 178; Gaps 23;
QY 50 KCOADPTC-SAAYVHLDSC-----TSSISTPLPS----- 77
DB 592 KCKNNPTCTSPQVMDADCECKCPKQKPGQCGDQKQKNDVRVCSGCVPRPDCTNGQ 651
QY 78 -----EPPSPVADCLEAAQQLNSLSIGCMCHRRMNQV-ACLDIYTWVHRA 123
DB 652 IYNINTCAGCGIDKPSCP-----KQIYNWKTCDCECPNGMKEPVGGCGAKTW----- 700

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QY 124 RSLGNVELDVSPYEDVTTSKP-----WKWNLKLNWLK----- 156
Db 701 -----LDDECCDCVPGKPGGGTGAQKWCNDKTKCKEKEKEMPTGGCENNNKMCDEFTC 753
QY 157 -----PDSDLCL-----KFAMLCITLNDKCDRLRKAYGEAGSGPHQRHVCRLQLLTFP 204
Db 754 DCVCPQKNTCIAPKWDATKSCICVNPCKNSPQVLKDTCCG--CQNVKSKCAPOKFI 811
QY 205 EKAAEPHAQGLLCPCA-PNDRGC-----GERRRNTIAPN 238
Db 812 EN-----ICDCACFNKQCKAPLVMSDBFCVCPNSGASMKTCLSPKEMNKTCT 861
QY 239 CALPPVAPNCLERLIC-----FSDPLCRSLRVDFQTHCHP-----WDILGTCAEBSRCL 289
Db 862 CDCNPPKPGC-----CPGTQKWMDDCKCGCPCNAQTDGAGKKFNDFTCSG-----CP 910
QY 290 RAYVLGLIGTAMTNFVSNVNTS-VALSCTCRSGNLOEBCMELEGFFSHNPCLTEAIAAK 348
Db 911 SGKLDCTG-----NTKWSAETCTC-GCGDVNRNGNKLXN-FNDNLQCEC-KNK 956
QY 349 MRPHSOLFQDMPHPTFAVNAH--QENENPAVRPQWPVPSLFSCTLP 392
Db 957 QEMANCKSPRTWNYDTCKVCCKNADSDDCVKPQIWLDDQCKGCP 1002

RESULT 5
T34264
Hypothetical protein F46C8.4 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C:Accession: T34264
R:Wilcox, L.
submitted to the EMBL Data Library, November 1995
A:Description: The sequence of C. elegans cosmid F46C8.
A:Reference number: Z21497
A:Accession: T34264
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-2195 <WIL>
A:Cross-references: UNIPARC:UPI000017B9D4; EMBL:U41624; PIDN:AAA83316.1; CESP:F46C8.4
C:Genetics:
A:Gene: CESP:F46C8.4
A:Introns: 19/3; 61/3; 80/1; 159/1; 182/1; 208/2; 246/1; 308/1; 367/1; 422/3; 466/1; 507/
629/3; 1721/3; 1767/3; 1811/1; 1874/1; 1920/1; 2011/2; 2068/3; 2117/1; 2161/1

Query Match 5.6%; Score 123.5; DB 2; Length 2195;
Best Local Similarity 23.0%; Pred. No. 0.17;
Matches 70; Conservative 37; Mismatches 105; Indels 93; Gaps 18;

QY 44 CLQARRKQAD-PTCSAAAYHLD-SCYSSISTPLPSEEPSVPADCLEAAQO----LRNSSL 98
Db 908 CAERNAQCQENYCTCRGTGTYNINGQCAANIVTP---AEPETLSQVKCMYQFLFLSPSGL 964
QY 99 IGCWC-----HRRMKNQVA-CLDIYVTVHARSGLNYELDVSPYEDVTTSKPKWKN 148
Db 965 LGHICTSNDRCKTAHSQCRNVQCIDGY-----RIFGSTQCIIRPG----- 1006
QY 149 LSKLNMLKPSDILCLFAMLCITLNDKCDRLRKAYGEAGS-GPHCORHVCRLQLLTFEKA 207
Db 1007 -----KPKRTERKESKLVELGDKCDKL-----SLCSKAICEKGVSCSP-ETFE-- 1051
QY 208 AEHPAQGLLCPAPNDRGCGERRRNTIAPNCALPPVAPNCLF-----LRLCPS 257
Db 1052 -----SDGAC---VKNVAKIKVVVPPLS-SCLOGEBCSGNSECVHGICF- 1091
QY 258 DPLCRSLRVDFQTHCHPMDILGTCAEQSCLRAYLGLIGTAMTNFVSN-----VNTSV 312
Db 1092 ----CKEFTLFEKGQRLRIIEKLTVLSESKL----IKPIKAHTTPTAASNTTIPVKYTT 1145
QY 313 ALSCT 317
Db 1146 TLQTT 1150
```

RESULT 6

A55567
fibrillin 1 - bovine
C:Species: Bos primigenius taurus (cattle)
C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C:Accession: A55567
R:Rilstra, D.J.; Li, L.; Potter, K.A.; Womack, J.; Byers, P.H.
Genomics 23, 480-485, 1994
A:Title: Sequence of the coding region of the bovine fibrillin cDNA and localization to
A:Reference number: A55567; MUID:95137597; PMID:7835900
A:Accession: A55567
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-2871 <TIL>
A:Cross-references: UNIPROT:P98133; UNIPARC:UPI000055AD2; GB:L28748; NID:G508427; PIDN
C:Superfamily: fibrillin; EGF homology
F:1201-1236/Domain: EGF homology <EGF>

Query Match 5.6%; Score 123.5; DB 2; Length 2871;

Best Local Similarity 19.3%; Pred. No. 0.22;
Matches 84; Conservative 46; Mismatches 131; Indels 175; Gaps 25;

QY 48 RRKCOADPTCSAAAYHLDSCYSSISTPLPSEEPSVPADCLEAAQQLRNSSLIG---CMC- 103
Db 2242 RRMCKDECEGKH-----DCAEKQMECKN--LIGTYLCIG 2277

QY 104 --HRRMKNQVACL-----IYVTVHARSGLNYELDVSPYEDVTTSKPKWKNLSKL 152
Db 2278 PGYQRRPDGEGCVDENECQTKPGICENGRCILNTRGTYTCECN---DGFTA----- 2324

QY 153 NMLKPDSDLCLK----FAMLCITLNDKC-----DLRKAYGEAGS-----GPHCORHVCL 197
Db 2325 ---SPNQCEDLNREGYCFTEVLQNMCOIGSNRNPVTKSECCDGGRGWGHPE--ICP 2379

QY 198 ROLLTFFKKAEPHAQGLL-----LC---PCAPNDRGCGERRRNTIAPNCA 240
Db 2380 FGQTVAFKLC-PhRGFWNGADIDECKVIHDCVNGECV-NDRG---SYHCICKGY 2433

QY 241 LPPVAPN-CLELRRICFSDP-----LCRSLRVDFQTHCHPMDI-----LGTCAE 284
Db 2434 TPDITGTACVDLINE-CNOAPKPCNFICKNTEGSCPKGYILOEDGRGSCDLDCAATK 2492

QY 285 QSRCLRAYLGLIGT---AMTNFVSN-----VNTSVALSCTC 318
Db 2493 QHNCQFLCVNTIGTSFTCKCPPGFTQHTTACIDNNECTSDINLCGSKGICQNTPGSFTCEC 2552

QY 319 R-----GSGNLQEECEML-----EGFFSH-----NPCL 341
Db 2553 QRGFSLDPTGASCDVDCEGHNRCQHGQNIIGGYRSCPGYLOHYQWNCVDENECL 2612

QY 342 TEAIAAKMRFHSQIFS 357
Db 2613 SAHICGGASCHNTLGS 2628

RESULT 7

A47221
fibrillin 1 precursor - human (fragment)

C:Species: Homo sapiens (man)
C>Date: 02-Jun-1995 #sequence_revision 25-Apr-1997 #text_change 31-Dec-2004
C:Accession: A47221; I54355; S17064; I59574; S17062; S62111; A34198

R:Corson, G.M.; Chaberg, S.C.; Dietz, H.C.; Charbonneau, N.L.; Sakai, L.Y.
Genomics 17, 476-484, 1993

A:Title: Fibrillin binds calcium and is coded by cDNAs that reveal a multidomain structure
A:Reference number: A47221; MUID:94010947; PMID:7691719

A:Accession: A47221

A:Molecule type: mRNA

A:Residues: 1-337, T', 339-1029 <COR>

A:Cross-references: UNIPROT:P35555; UNIPROT:Q15972; UNIPROT:Q9NP01; UNIPARC:UPI000017651
R:Pereira, L.V.; D'Alessio, M.; Ramirez, F.; Lynch, J.; Sykes, B.; Pangilinan, T.; Bona
Hum. Mol. Genet. 2, 961-968, 1993

A;Title: Genomic organization of the sequence coding for fibrillin, the defective gene p
A;Reference number: 154355; MUID:93372860; PMID:8364578
A;Accession: I54355
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 132-3002 <PER>
A;Cross-references: UNIPARC:UPI0000055AD1; GB:L13923; NID:9306745; PIDN:AB02036.1; PID:
R;Maslen, C.L.; Corson, G.M.; Maddox, B.K.; Glanville, R.W.; Sakai, L.Y.
Nature 352, 334-337, 1991
A;Title: Partial sequence of a candidate gene for the Marfan syndrome.
A;Reference number: S17064; MUID:91304568; PMID:1852207
A;Accession: S17064
A;Molecule type: mRNA
A;Residues: 1030-3002 <MAS>
A;Cross-references: UNIPARC:UPI0000176517; EMBL:X63556
R;Dietz, H.C.; Valle, D.; Francomano, C.A.; Kendzior, R.J.
Science 259, 680-683, 1993
A;Title: The skipping of constitutive exons in vivo induced by nonsense mutations.
A;Reference number: I59574; MUID:93157831; PMID:8430317
A;Accession: I59574
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 2217-2288, 'I', 2290-2325 <RES>
A;Cross-references: UNIPARC:UPI000006FPF6; GB:S54426; NID:9264860; PIDN:AB25244.1; PID:
R;Lee, B.; Godfrey, M.; Vitale, E.; Hori, H.; Mattei, M.G.; Sarfarazi, M.; Tsipouras, P.
Nature 352, 330-334, 1991
A;Title: Linkage of Marfan syndrome and a phenotypically related disorder to two different
A;Reference number: S17062; MUID:91304567; PMID:1852206
A;Accession: S17062
A;Molecule type: mRNA
A;Residues: 'VLVTVVFILSNKWL', 944-1444 <LEE1>
A;Cross-references: UNIPARC:UPI0000072A79; EMBL:X62008; NID:G31398; PIDN:CAB56534.1; PID:
A;Accession: S62111
A;Molecule type: protein
A;Residues: 1166-1176, 'Y', 1178-1180, 'D', 1182-1185 <LEE2>
A;Cross-references: UNIPARC:UPI0000176518
R;Maddox, B.K.; Sakai, L.Y.; Keene, D.R.; Glanville, R.W.
J. Biol. Chem. 264, 21381-21385, 1989
A;Title: Connective tissue microfibrils. Isolation and characterization of three large p
A;Reference number: A34198; MUID:90078246; PMID:2512293
A;Accession: A34198
A;Molecule type: protein
A;Residues: 565-575/1890-1892, 'I', 1894-1900 <MAD>
A;Cross-references: UNIPARC:UPI0000176519; UNIPARC:UPI000017651A
C;Comment: Fibrillin is a major component of elastin-associated microfibrils.
C;Genetics:
A;Gene: GDB:FBN1
A;Cross-references: GDB:127115; OMIM:134797; OMIM:154700
A;Map position: 15q21.1-15q21.1
A;Introns: 2236/1; 2258/1; 2297/1
C;Superfamily: EGF homology
F;1-3002/Product: fibrillin (5'-region exon A splice form) #status predicted <MAD>
F;132-3002/Product: fibrillin (5'-region exon C splice form) #status predicted <MAD>
F;1332-1367/Domain: EGF homology <EGF>
F;1457-1492/Domain: EGF homology <EGF2>
F;2262-2295/Domain: EGF homology <EGF1>

Query Match 5.68; Score 123.5; DB 2; Length 3002;
Best Local Similarity 19.34; Pred. No. 0.23;
Matches 84; Conservative 46; Mismatches 131; Indels 175; Gaps 25;

QY 48 RRKQADPTCSAAVHLDSDTSSTISPLPSEPSVPADCLEAAQRLNSSLIG---CMC- 103
DB 2373 RMCKDEDEEKGK-----DCTEKQNECKN--LIGTYMCIG 2408

QY 104 --HRRMKNQVACL-----IYWTVTHARSIGNYELDVSPYEDVTTSKPMKNLSKL 152
DB 2409 PGYQRPDGGGVDENECQTKPGICENGRCNLTGRGVTTCEN---DGFTA----- 2455

QY 153 NMLKPDSDCLCK-----FAMLCNLNDKC-----DLRKYAGEAS-----GPHCQRHVCL 197
DB 2456 ---SPNQDECLDNREGYCFTEVLQNMCMQIGSSNRNPVTKSECCDGGRGWGPCHC--ICP 2510

QY 198 RQLLTFFEKAAEPHAQGL-----LC-----PCAPNDRGCGERRRNTIAPNCA 240
DB 2511 FQGTVAFFKLC- PHERGFWTNGADIDBECKVIHVDVCRNGECV-NDRG---SYHCICKTGY 2564

QY 241 LPVV-APNCLLELRRLCFSDP-----LCRSLVDVPOTHCHPMDI-----LGTGATE 284
DB 2565 TPDIITGTCVDLNE-CNAPKPCNFICKNTEGYSQCSPKGYLQEDGRSKOLDDECATK 2623

QY 285 QSRCLRAYLGLIG--TAMTPNPFVN-----VNTSVALSCTC 318
DB 2624 QHNCQFLCVNTIGGFTCKCPFGTQHTSCIDNNECTSDINLCGSKGICQNTPGSFCEC 2683

QY 319 R-----GSGNMQEECEML-----EGFFSH-----NPCL 341
DB 2684 QRGFSLDQGTSSCEDVDECEGNHRCQHGQNIIGYRCSCPGYQLHYQWQNCVDENECL 2743

QY 342 TEAIAAKMRPHSOLF 357
DB 2744 SAHICGGASCHNTLGS 2759

RESULT 8
T09059
notch4 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession: T09059
R;Rowen, L.; Mahairas, G.; Qin, S.; Ahearn, M.E.; Dankers, C.; Lasky, S.; Loretz, C.;
submitted to the EMBL Data Library, October 1997
A;Description: Sequence of the mouse major histocompatibility locus class III region.
A;Reference number: Z16543
A;Accession: T09059
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-1964 <ROW>
A;Cross-references: UNIPROT:P31695; UNIPARC:UPI000016C7F1; EMBL:AF030001; NID:92564945;
C;Genetics:
A;Gene: notch4
A;Map position: 17
A;Introns: 22/1; 49/2; 148/1; 264/1; 305/1; 384/1; 436/1; 501/1; 539/1; 577/1; 618/1; 619/1;
1679/3; 1729/1; 1761/3
C;Superfamily: notch protein; ankyrin repeat homology; EGF homology
C;Keywords: receptor; signal transduction
P;514-545/Domain: EGF homology <EGF>

Query Match 5.58; Score 120; DB 2; Length 1964;
Best Local Similarity 22.86; Pred. No. 0.28;
Matches 81; Conservative 30; Mismatches 135; Indels 112; Gaps 22;

QY 51 CQADPTCSAAVHLDSDTSSTISPLPSEPSVPADCLEAAQRLNSSLIGCMC----- 103
DB 417 CQPGYSGSTCHQDLDESCWAQQGSP-----CEHGSGCINTPGSFNCLCLPGVTGS 467

QY 104 -----HRRMKNQ-----VACLDIYWTVTHARSIG-----NYELDVSPYEDVTTSKPMKNL 149
DB 468 RCEADHNECLSQCPHGSTCLDLATFHLCPGLEGRLECEVEV-----NECTSNPCLNQA 523

QY 150 SKLNLKPDSDCLCK--FAMLCNLN-DKCDRLKAYGEAC-----SGPHC 191
DB 524 ACHDLLNGFQCLCLPGFTGARCEKMDCECSSTPCANGRCRDQPGAFYCECLPGFEGPHC 583

QY 192 QRHV-----CLRQLLTFFEKAAEPHAQGL-----LCP---CAPNDRGGGERR 231
DB 584 EKEVDECLSDPCPVGASCLDLPGAFP-CLCRPQFTQQLCEVPLCTNMCPGQCGOQOE 642

QY 232 RNTIAPNCLAPPVAPNCLLEL-----RRLCFSD-----PLCRSLVD-FQTHC- 272
DB 643 R---AP-CLCPDGSPCVPAEDNCPCHGHCORSLCVCDEGWGTGPECETELGCGISTPCA 698

QY 273 HPMIDLGTCAEQS-----RCLRAYLGI-----IGTAMTFVSNVNTSV---ALSTCTC 318
DB 699 HG-----GTCHPQSPGYNCTCPAGYMLTCEEVTAHSGCLNGGSGCIRPEGSCTC 752

A/Accession: B46438
A/Status: preliminary
A/Molecule type: nucleic acid
A/Residues: 1865-1932, 'RR', 1935-1937, 'L', 1938-1967, 'I', 1969-2044, 'IE', 2047-2052, 'S', 2054
A/Cross-references: UNIPARC:UPI0000177463
A/Experimental source: embryo
A/Note: sequence extracted from NCBI backbone (NCBIN:131246, NCBIPI:131247)
C/Comment: This protein has many EGF repeats and lin-12[1172]/Notch repeats.
C/Comment: This protein is one of the neurogenic proteins controlling the decision between
C/Genetics:
A/Gene: notch-1
A/Map position: 2
A/Note: proximal region of chromosome 2
C/Superfamily: notch protein; ankyrin repeat homology; EGF homology
F/106-138/Domain: EGF homology <EGF1>
F/144-175/Domain: EGF homology <EGF1>
F/222-254/Domain: EGF homology <EGF2>
F/261-292/Domain: EGF homology <EGF2>
F/339-370/Domain: EGF homology <EGF3>
F/416-449/Domain: EGF homology <EGF3>
F/456-487/Domain: EGF homology <EGF3>
F/494-525/Domain: EGF homology <EGF3>
F/532-563/Domain: EGF homology <EGF6>
F/607-638/Domain: EGF homology <EGF7>
F/682-713/Domain: EGF homology <EGF8>
F/757-788/Domain: EGF homology <EGF9>
F/795-826/Domain: EGF homology <EGF10>
F/873-904/Domain: EGF homology <EGF11>
F/911-942/Domain: EGF homology <EGF12>
F/949-980/Domain: EGF homology <EGF13>
F/987-1018/Domain: EGF homology <EGF14>
F/1025-1056/Domain: EGF homology <EGF15>
F/1063-1094/Domain: EGF homology <EGF16>
F/1149-1180/Domain: EGF homology <EGF17>
F/1187-1218/Domain: EGF homology <EGF18>
F/1233-1264/Domain: EGF homology <EGF19>
F/1352-1383/Domain: EGF homology <EGF19>
F/1391-1425/Domain: EGF homology <EGF>
F/1917-1948/Domain: ankyrin repeat homology <AN1>
F/1949-1981/Domain: ankyrin repeat homology <AN2>
F/1983-2015/Domain: ankyrin repeat homology <AN3>
F/2016-2048/Domain: ankyrin repeat homology <AN4>
F/2049-2081/Domain: ankyrin repeat homology <AN5>

RESULT 12
T42215
zonadhesin - mouse
N/Alternate names: sperm-specific membrane protein
C/Species: Mus musculus (house mouse)
C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C/Accession: T42215
R/Gao, Z.; Garbers, D.L.
J. Biol. Chem. 273, 3415-3421, 1998
A/Title: Species diversity in the structure of zonadhesin, a sperm-specific membrane protein
A/Reference number: Z22080; MUID:98123114; PMID:9452463
A/Accession: T42215
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-5376 <GAO>
A/Cross-references: UNIPROT:O88799; UNIPARC:UPI000002A15B; EMBL:U97068; NID:G3327420; P
C/Genetics:
A/Gene: Zan
A/Map position: 5
C/Function:
A/Description: functions in multiple cell adhesion processes
A/Note: found exclusively on the apical region of the sperm head
C/Keywords: cell adhesion

Query Match 5.3%; Score 115; DB 2; Length 5376;
Best Local Similarity 21.1%; Pred. No. 2;
Matches 80; Conservative 30; Mismatches 132; Indels 138; Gaps 19;
QY 42 NSCLQARRKQADPTCSAAYHHLDSCSTSSISTPLPSEERSVPADCLEAAQQLNSSLIGC 101
Db 3291 SNCTEITLQC---PTNSQFTDCLPSCVPCSNRCRVTSPSPSSCRE-----GC 3336
QY 102 MCHRRM-----KNQVACLDIYVTVHRRASLGNLYELDVSPYEDYTVTSKPWKM----- 147
Db 3337 LCNHGFVPSDEKCVPTQCGKD-----ARGA-----IIPAGTWTISKGCTQSCACV 3383
QY 148 --NLSKLNMLKP-----DSDLCLKPFAMLTINDK-----PNCALPPVAPNCLERLRC- 255
Db 3384 EGNIOQNFQCPPEYCKDNSEGSTCTKITLQCPAHTQVTSCLPCLSPCLDPEGLCKD 3443
QY 178 LRKAYGEAC-SGPHQQRHVCLRLQLLTFFFEKAAE-PHAQGLL----- 217
Db 3444 ISPKVPSTCKEGCVCQSGVYLNDSKCVLRAEDCKDAQALIPAGKTWTSPGCTQSCACM 3503
QY 218 -----CP-----CAPNDRGCGERRNTIA-----PNCALPPVAPNCLERLRC- 255
Db 3504 GGAVQCQSSQCPPTGYCKDNEDGNSNCAKITLQCPAHSFTNC-LPFCPLSPCLDPEGLCK 3562
QY 256 FSDP-----LCRSRLVDFQTHCHPMDILGTCAEQSCLRAYLGLIGTAMTPNFV 305
Db 3563 GASPKVPSTCKEGCICQSGVYLNDSKCVLRAEDCKDAQALIPAGKTWTSPGCTQSCACM 3609
QY 306 SNVNTSVALSCYCRSGNLIQ 325
Db 3610 TWSRGCTQSCVCTG-GSIQ 3628

RESULT 13
T44598
hypothetical protein [imported] - fruit fly (Drosophila melanogaster)
N/Alternate names: BcDNA.LD22726
C/Species: Drosophila melanogaster
C/Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 17-Nov-2000
C/Accession: T44598
R/Rubin, G.M.; Wan, K.H.; Harvey, D.; Lewis, S.E.; Brokstein, P.; Tsang, G.; Agbayani, M.
n. D.E.; Frise, E.; Galle, R.; George, R.A.; Harris, N.L.; Hoskins, R.A.; Evans-Holm, M.
; Snit, E.; Svirskas, R.R.; Weinburg, T.; Celnikier, S.E.
submitted to the EMBL Data Library, April 1999
A/Reference number: Z22805
A/Accession: T44598
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-1106 <RUB>

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GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 12, 2006, 02:00:03 ; Search time 154.078 Seconds
(without alignments)
1831.616 Million cell updates/sec

Title: US-10-668-936-21
Perfect score: 2190
Sequence: 1 MVRPLNRPPLPPVLMLLL.....PWVPSLFSTPLLLLSLW 400

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2190	100.0	400	1	GFR33 HUMAN
2	1646.5	75.2	397	1	GFR33 MOUSE
3	1642.5	75.0	397	2	Q6AXR3 RAT
4	1628	74.3	385	2	Q9R2D0 MOUSE
5	1051	48.0	222	2	Q9QZG2 RAT
6	568	25.9	465	1	GFR33 CHICK
7	545.5	24.9	463	2	Q920Y3 MOUSE
8	544.5	24.9	464	2	Q5E9X0 BOVIN
9	544.5	24.9	463	1	GFR33 MOUSE
10	542.5	24.8	444	2	Q792X9 RAT
11	542.5	24.8	464	2	Q35977 RAT
12	540.5	24.7	460	2	Q5REZ9 PONPY
13	540.5	24.7	464	1	GFR33 HUMAN
14	540.5	24.7	464	2	Q6GTR9 HUMAN
15	540.5	24.7	464	2	Q5RAD6 PONPY
16	536.5	24.5	469	1	GFR33 CHICK
17	530.5	24.2	464	2	Q5R9T3 PONPY
18	529.5	24.2	431	2	Q4RGH8 TETNG
19	522.5	23.9	472	2	Q9HTT9 BRARE
20	516	23.6	465	1	GFR33 HUMAN
21	514.5	23.5	463	2	Q35252 MOUSE
22	513	23.4	468	1	GFR33 MOUSE
23	513	23.4	468	2	Q35246 MOUSE
24	512.5	23.4	463	2	Q35748 RAT
25	511	23.3	468	1	GFR33 RAT
26	504	23.0	481	2	Q9HTT8 BRARE
27	497.5	22.7	431	1	GFR33 CHICK
28	496	22.6	333	2	Q4RTG0 TETNG
29	482.5	22.0	495	2	Q6TSC3 BRARE
30	474.5	21.7	342	2	Q4SDM1 TETNG
31	454.5	20.8	484	2	Q4S1R4 TETNG

32	418.5	19.1	358	2	Q922A3 MOUSE
33	412.5	18.8	359	2	Q58J92 HUMAN
34	408	18.6	330	2	Q922A2 MOUSE
35	406	18.5	203	2	Q4SPK7 TETNG
36	361.5	16.5	260	1	GFR33 MOUSE
37	361	16.5	273	1	GFR33 RAT
38	296.5	13.5	299	1	GFR33 HUMAN
39	296.5	13.5	299	2	Q5JT74 HUMAN
40	275.5	12.6	247	2	Q4SG83 TETNG
41	257.5	11.8	182	2	Q5JT77 HUMAN
42	220	10.0	394	2	Q6UXV0 HUMAN
43	219	10.0	393	2	Q6SJE0 MOUSE
44	210	9.6	225	2	Q9QWK2 MOUSE
45	184.5	8.4	109	2	Q8JG58 AMBME

ALIGNMENTS

RESULT 1

GFR33 HUMAN STANDARD; PRT; 400 AA.

AC 060603, Q6UW20; Q8IUZ2;

DT 16-OCT-2001 (Rel. 40, Created)

DT 25-OCT-2004 (Rel. 45, Last sequence update)

DT 13-SEP-2005 (Rel. 48, Last annotation update)

DE GDNF family receptor alpha 3 precursor (GFR-alpha 3) (GFRalpha3).

GN Name=GFR33; ORFName=UNQ3339/PRO538/PRO3664;

OS Homo sapiens (Human)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;

OC Homo.

OX NCBI_TaxID=9606;

LN [1]

RP NUCLEOTIDE SEQUENCE (ISOFORM 1), AND TISSUE SPECIFICITY.

RA MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;

RA Baloh R.H., Gorodinsky A., Golden J.P., Tansey M.G., Keck C.L.,

RA Popescu N.C., Johnson E.M. Jr., Milbrandt J.,

RA "GFRalpha3 is an orphan member of the GDNF/neurturin/persephin

RT receptor family."

RL Proc. Natl. Acad. Sci. U.S.A. 95:5801-5806 (1998).

RN [2]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORMS 1 AND 2).

RA MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;

RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D.T., Brush J.,

RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,

RA Eaton D., Foster J.S., Grimaldi C., Gu Q., Hass P.E., Heldens S.,

RA Huang A., Kim H.S., Kimowski L., Jin Y., Johnson S., Lee J.,

RA Lewis L., Liao D., Mark M.R., Robbie E., Sanchez C., Schoenfeld J.,

RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,

RA Vandlen R.L., Watanabe C., Wieand D., Woods K., Xie M.-H.,

RA Yaneura D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A.D.,

RA Wood W.I., Godowski P.J., Gray A.M.,

RA "The secreted protein discovery initiative (SPDI), a large-scale

RT effort to identify novel human secreted and transmembrane proteins: a

RL bioinformatics assessment."

RN [3]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).

RA TISSUE=Pancreas;

RA MEDLINE=22398257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Klausner R.D., Collins F.S., Wagner L.H., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [4]
 RN PROTEIN SEQUENCE OF 32-46.
 RP PubMed=15340161; DOI=10.1110/ps.04682504;
 RX Zhang Z., Henzel W.J.;
 RA "Signal peptide prediction based on analysis of experimentally
 RT verified cleavage sites";
 RL Protein Sci. 13:2819-2824(2004).
 RN [5]
 RN FUNCTION.
 RP MEDLINE=99098192; PubMed=9883723; DOI=10.1016/S0896-6273(00)80649-2;
 RA Baloh R.H., Tansey M.G., Lampe P.A., Fahrner T.J., Enomoto H.,
 RA Simburger K.S., Leitner M.L., Araki T., Johnson E.M. Jr.,
 RA Milbrandt J.;
 RT "Artemin, a novel member of the GDNF ligand family, supports
 RT peripheral and central neurons and signals through the GFRalpha3-RET
 RT receptor complex";
 RL Neuron 21:1291-1302(1998).
 CC -1- FUNCTION: Receptor for the glial cell line-derived neurotrophic
 CC factor, artemin. Mediates the artemin-induced autophosphorylation
 CC and activation of the RET receptor tyrosine kinase.
 CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=O60609-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=O60609-2; Sequence=VSP_010942;
 CC -1- TISSUE SPECIFICITY: Widely expressed in adult and fetus which
 CC exhibit a similar pattern. Essentially not expressed in the
 CC central nervous system, but highly expressed in several sensory
 CC and sympathetic ganglia of the peripheral nervous system. Moderate
 CC expression in many nonneuronal tissues, particularly those of the
 CC digestive and urogenital systems, but high expression in stomach
 CC and appendix. Several types of glandular tissues show low
 CC expression. Very low or no expression detected in the
 CC hematopoietic system.
 CC -1- SIMILARITY: Belongs to the GDNFR family.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 CC EMBL; AF051767; AAC24355.1; -; mRNA.
 CC EMBL; AV358997; AAQ89356.1; -; mRNA.
 CC EMBL; AV359037; AAQ89396.1; -; mRNA.
 CC EMBL; BC037951; AAH37951.1; -; mRNA.
 CC EMBL; ENSG00000146013; Homo sapiens.
 CC HGNC; HGNC:4245; GFRA3.
 CC MIM; 605710; -.
 CC GO; GO:0019898; TAS.
 CC GO; GO:0005102; F:receptor binding; TAS.
 CC GO; GO:0007422; P:peripheral nervous system development; TAS.
 CC GO; GO:0007165; P:signal transduction; TAS.
 CC InterPro; IPR003438; GDNF_receptor.
 CC InterPro; IPR003505; GDNF_receptor3.
 CC PANTHER; PTHR10269; GDNF_Receptor; 1.
 CC Pfam; PF02351; GDNF; 1.
 CC PRINTS; PR01319; GDNFRALPHA3.
 CC PRINTS; PR01316; GDNFRECEPTOR.
 KW Alternative splicing; Direct protein sequencing; Glycoprotein;
 KW GPI-anchor; Lipoprotein; Membrane; Receptor; Signal.
 FT SIGNAL 1 31
 FT CHAIN 32 374 GDNF family receptor alpha 3.

FT PROPEP 375 400 Removed in mature form (Potential).
 FT LIPID 374 374 GPI-anchor amidated asparagine
 FT (Potential).
 FT CARBOHYD 95 95 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 148 148 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 309 309 N-linked (GlcNAc...) (Potential).
 FT VARSPLIC 127 157 Missing in isoform 2).
 FT /FTId=VSP_010942.
 FT CONFLICT 108 108 K -> R (in Ref. 1).
 SQ SEQUENCE 400 AA; 44511 MW; B0BC252FE1F072C7 CRC64;
 Query Match 100.0%; Score 2190; DB 1; Length 400;
 Best Local Similarity 100.0%; Pred. No. 7.9e-168;
 Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MVRPLNRPPLPPVLMMLLLLLPPSPPLAAGDPLPTESLMNSCLQARRKQADPTCSAA 60
 DB 1 MVRPLNRPPLPPVLMMLLLLLPPSPPLAAGDPLPTESLMNSCLQARRKQADPTCSAA 60
 QY 61 YHLDSTSSISTPLPSPSPVPADCLEAAQQLRNSLLIGCMCHRRMKQVACLDIYWTV 120
 DB 61 YHLDSTSSISTPLPSPSPVPADCLEAAQQLRNSLLIGCMCHRRMKQVACLDIYWTV 120
 QY 121 HRASIGNYELDVSPYEDVTVTSKPMKNLSKLNMLKPDSDCLCKFAMLTCLNDKCDRLRK 180
 DB 121 HRASIGNYELDVSPYEDVTVTSKPMKNLSKLNMLKPDSDCLCKFAMLTCLNDKCDRLRK 180
 QY 181 AYGEACSGPHCQRHVCLRLQLLTFFKAAEPHAQGLLLCPANDRGCGRRRTIAPNCA 240
 DB 181 AYGEACSGPHCQRHVCLRLQLLTFFKAAEPHAQGLLLCPANDRGCGRRRTIAPNCA 240
 QY 241 LPPVAPNCLRLRRLCFSDPLCRSLRVDFTCHPMDILGTCAEQSRCLRAYLGLIGTAM 300
 DB 241 LPPVAPNCLRLRRLCFSDPLCRSLRVDFTCHPMDILGTCAEQSRCLRAYLGLIGTAM 300
 QY 301 TPNFVSNVNTSVALSCTCRGSGNLQECMELEGFHSHNFCPLTEAIAAKRFRHSQSFQDW 360
 DB 301 TPNFVSNVNTSVALSCTCRGSGNLQECMELEGFHSHNFCPLTEAIAAKRFRHSQSFQDW 360
 QY 361 PHTPTFVMAHQENPAVRPQWPVPSLFTPLILLLSLW 400
 DB 361 PHTPTFVMAHQENPAVRPQWPVPSLFTPLILLLSLW 400
 RESULT 2
 GFRA3_MOUSE STANDARD; PRT; 397 AA.
 ID GFRA3_MOUSE 035325; O55243; Q6NZC2; Q8C8L9;
 AC 035118; O35325; O55243; Q6NZC2; Q8C8L9;
 DT 25-OCT-2004 (Rel. 45, Created)
 DT 25-OCT-2004 (Rel. 45, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE GDNF family receptor alpha 3 precursor (GFR-alpha 3) (GFRA3pha3).
 GN Names=GFra3;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Muridae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RN NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6; TISSUE=Heart;
 RX MEDLINE=98205811; PubMed=9535755; DOI=10.1006/bbrc.1998.8361;
 RA Nomoto S., Ito S., Yang L.-X., Kiuchi K.;
 RT "Molecular cloning and expression analysis of GFR alpha-3, a novel
 RT cDNA related to GDNFR alpha and NTR-alpha".
 RL Biochem. Biophys. Res. Commun. 244:849-853(1998).
 RN [2]
 RN NUCLEOTIDE SEQUENCE.
 RX MEDLINE=98420233; PubMed=9749804;
 RA Widenfalk J., Tomac A., Lindqvist E., Hoffer B., Olson L.;
 RT "GFRalpha-3, a protein related to GFRalpha-1, is expressed in
 RT developing peripheral neurons and ensheathing cells".
 RL Eur. J. Neurosci. 10:1508-1517(1998).

QY 189 PHCQRHVLCRLQLTFFPKAAEPHAQGLLCPAPNDRCGERRNTIAPNCALPPVAPNC 248
 DB 186 IRCORHLCLAQRLSFFPKAAESHAQGLLCPAPNDRCGERRNTIAPNCALPPVAPNC 245
 QY 249 LEIRLRCFSDPLCRSLRVDFOHCHPMDILGTCAEQSLRAYLGLIGTAMTNPVSVN 308
 DB 246 LDRSFCRADPLCRSLRVDFOHCHPMDILGTCAEQSLRAYLGLIGTAMTNPVSVN 305
 QY 309 NTSVALSCTCRSGNLQCEMLEGFFSHNPCLTEIAAAMRPHSOLFQSDMPHPTFFAYM 368
 DB 306 NTSVALSCTCRSGNLQCEMLEGFFSHNPCLTEIAAAMRPHSOLFQSDMPHPTFFAYM 365
 QY 369 AHQONENPAVRPQWVPSLFTPLILLISLW 400
 DB 366 QOQNSNPALRLOPLRPLSILPLILLQTLW 397

RESULT 3
 Q6AXR3 RAT PRELIMINARY; PRT; 397 AA.
 AC Q6AXR3;
 DT 25-OCT-2004 (T-EMBLrel. 28, Created)
 DT 25-OCT-2004 (T-EMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (T-EMBLrel. 28, Last annotation update)
 DE Glial cell line derived neurotrophic factor family receptor alpha
 GN 3.
 DE Name=Gfra3;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Kidney;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.F., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan A., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ueidi T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Kidney;
 RG NIH MGC Project;
 RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC079378; AAH79378.1; -, mRNA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR InterPro; IPR003438; GDNF receptor.
 DR InterPro; IPR003505; GDNF_receptorA3.
 DR Pfam; PF02351; GDNF; 1.
 DR PRINTS; PR01319; GDNFRALPHA3.
 DR PRINTS; PR01316; GDNFRECEPTOR.
 KW Receptor.
 SQ SEQUENCE 397 AA; 44053 MW; E11D2E7B9CB46AF8 CRC64;

Query Match 75.08; Score 1642.5; DB 2; Length 397;

Best Local Similarity 77.2%; Pred. No. 9e-124;
 Matches 305; Conservative 30; Mismatches 57; Indels 3; Gaps 1;
 QY 6 NRPPLPPVVLMLLLPLPSPLPLAAGDPLPTSRMLNSCLQARRKQADPTCSAAHYHLD 65
 DB 6 SPRPPLVILLVLSL--WLPGLTGNLSPTENRLVNSCTQARKKEANPACKAAAYQHLD 62
 QY 66 STTSISITPLSEEPSVPADCLAAQQLNSSLIGCMCHRRMKNQVACLDIYTVTHRAS 125
 DB 63 SCTPLSSPLPSGESATSAACLEAAQQLNSSLIDCRHRRMKHQTCLDIYTVTHPVRS 122
 QY 126 LGNYELDVSPYEDTIVTSKPKWKNLKLKMLKPDSDLCKFAMLCTLNDKCDRLRKAYGEA 185
 DB 123 LGDYELDVSPYEDTIVTSKPKWKNLKLKMLKPDSDLCKFAMLCTLNDKCDRLRKAYGEA 182
 QY 186 CSGPHICQHVLCRLQLTFFPKAAEPHAQGLLCPAPNDRCGERRNTIAPNCALPPVPA 245
 DB 183 CSGIRQCRLCLAQRLSFFPKAAESHAQGLLCPAPNDRCGERRNTIAPNCALPPVPA 242
 QY 246 PNCLELRRLCFSDPLCRSLRVDFOHCHPMDILGTCAEQSLRAYLGLIGTAMTNPV 305
 DB 243 PNCLELRRLCFSDPLCRSLRVDFOHCHPMDILGTCAEQSLRAYLGLIGTAMTNPV 302
 QY 306 SNVNTSVALSCTCRSGNLQCEMLEGFFSHNPCLTEIAAAMRPHSOLFQSDMPHPTFF 365
 DB 303 SKVNTVALGCTCRSGNLQCEMLEGFFSHNPCLTEIAAAMRPHSOLFQSDMPHPTFF 362
 QY 366 AVMAHONENPAVRPQWVPSLFTPLILLISLW 400
 DB 363 SVMQOQNSNPALRLOPLRPLSILPLILLQTLW 397

RESULT 4
 Q9R2D0 MOUSE PRELIMINARY; PRT; 385 AA.
 AC Q9R2D0;
 DT 01-MAY-2000 (T-EMBLrel. 13, Created)
 DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
 DE TGF-beta-related neurotrophic receptor-3 precursor.
 GN Name=Gfra3; Synonyms=TrnR-3;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Swiss-Webster /NIH; TISSUE=Embryo;
 RA Zhong J., Annies M., Tolle A., Heumann R.;
 RT "Molecular cloning of a new member of TrnR family.";
 RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; Y15110; CAAY5384.1; -, mRNA.
 DR MGI; MGI:1201403; Gfra3.
 DR GO; GO:0005615; C:extracellular space; TAS.
 DR GO; GO:0008046; F:axon guidance receptor activity; IMP.
 DR GO; GO:0015026; F:coreceptor activity; TAS.
 DR GO; GO:0005515; F:protein binding; IPI.
 DR GO; GO:0007411; P:axon guidance; IMP.
 DR GO; GO:0007422; P:peripheral nervous system development; IMP.
 DR GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. .; TAS.
 DR InterPro; IPR003438; GDNF receptor.
 DR InterPro; IPR003505; GDNF_receptorA3.
 DR Pfam; PF02351; GDNF; 1.
 DR PRINTS; PR01319; GDNFRALPHA3.
 DR PRINTS; PR01316; GDNFRECEPTOR.
 KW Receptor; Signal.
 FT SIGNAL 1 15 Potential.
 SQ SEQUENCE 385 AA; 42997 MW; 91A7F3P9FF30ED14 CRC64;

Query Match 74.3%; Score 1628; DB 2; Length 385;
 Best Local Similarity 77.9%; Pred. No. 1.3e-122;
 Matches 300; Conservative 29; Mismatches 56; Indels 0; Gaps 0;


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19  LLLPPSPPLAAGDPLPTES----RLMNSCLQARRKQADPTCSAAHYHLDSTS--SIS 72
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
20  LAAPSP-----PQDILQGHVWPVDCIRANKLCAEAGSCSSRYTIRLOCLAGDRN 70
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
73  TPLPEEPSVPADCLAEAAQOLRNSLIGCMCHRRMKQVACLDIYTVHRRASLGNYEYD 132
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
71  TWLANKE-----CQAALEVLQESPLYDCRCRGMWKEIQCLQVYWSIHLGAEGEFYE 124
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
133  VSPYEDTVTSKPKWNLSKLANL-----KPSDLCLKFAMLCNTNDKCDRLKA 181
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
125  ASPEY-PITSR-----LSDIFRLASIFSGMDPATNSKSNHCLDAAKACNLNDNCKLRSG 178
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
182  YGEACS-----GPHCORHVLCROLLTPEKAAEPHAQGLLCCAPNDRCGGERRENTIA 236
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
179  YISTCSKEISATEHCSRKCKHAKLRQFPDNPVSPSYTYRLLFCSC--KQQAEPFRQTV 236
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
237  PNICAL-PPVAPNCLERLFCSPDLCKSRLLVDFQTHC-PMDILGTCAEQ-SRCLRAYL 293
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
237  PFCSEYDKEKNCLDRNVCRADHLCKRSLADFIANCAQSFQSLTSCPGNYOACLGSYT 296
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
294  GLIGTAMTFNFSVNTYVALS--CTCRGSGNLOEECEMLEGFFSHNPJCITEAIAAMRF 351
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
297  GLIGDMTFNYDASTTISITSPWCSCKGSGNLEECEKFLRDTFNPCLRNAIQFNGNG 356
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
352  HSOLFSDQWHPHTFAVMAHQENPAV 377
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
357  TDVNLSPKPNPSPPIITMLPKVKEKSPAL 382
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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RESULT 7
Q920Y3 MOUSE Q920Y3 MOUSE PRELIMINARY; PRT; 463 AA.
AC Q920Y3;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Glial cell line derived neurotrophic factor family receptor alpha
2.
GN Name=Gfra2;
GN Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL;
RC MEDLINE=22711886; PubMed=12829325; DOI=10.1016/S0169-328X(03)00169-4;
RX "Too H.P.;
RT Real time PCR quantification of Gfra2 alternatively spliced
RT isoforms in murine brain and peripheral tissues.";
RL Brain Res. Mol. Brain Res. 114:146-153(2003).
[2]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL;
RC Wong Y.W., Too H.P.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR ENBL; AF398416; AAK97483.1; -; Genomic DNA.
DR ENBL; AF398411; AAK97483.1; JOINED; Genomic DNA.
DR ENBL; AF398412; AAK97483.1; JOINED; Genomic DNA.
DR ENBL; AF398414; AAK97483.1; JOINED; Genomic DNA.
DR ENBL; AF398415; AAK97483.1; JOINED; Genomic DNA.
DR ENBL; AF398413; AAK97483.1; JOINED; Genomic DNA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR003438; GDNF_receptor.
DR InterPro; IPR003504; GDNF_receptorA2.
DR Pfam; PF02351; GDNF; 1
DR PRINTS; PR01316; GDNFRALPHA2.
DR PRINTS; PR01316; GDNFRECEPTOR.
DR Receptor.
SQ SEQUENCE 463 AA; 51582 MW; 42FAA1EF59975E2C CRC64;

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FT CONFLICT 462 462 Q -> L (in Ref. 3).
SQ SEQUENCE 464 AA; 51559 MW; 8BC604D9530FF21F CRC64;

Query Match 24.7%; Score 540.5; DB 1; Length 464;
Best Local Similarity 36.5%; Pred. No. 5.2e-35;
Matches 120; Conservative 47; Mismatches 123; Indels 39; Gaps 10;

QY 44 CLOARRKCOADPTCSAAVHLDSCYS--SISPLSEEPSVPADCLEAAQQLRNSSLIGC 101
DB 40 CVRANELCAESNCSRYRTLQCLAGDRDNTMLANKE-----COAALEVLQESPLYDC 93

QY 102 MCHRRMKNQVACLIDYWTVHRARSIGNYELDVSPYEDVTTSKPKWNLNLSKL----- 152
DB 94 RCKRGMKKELQCLQIYWSIHGLGTEGEFFYEASPYE--PVTSR-----LSDIFRLASIFSG 147

QY 153 -----NMLKPDSDLCIKFAMLCITLNDKDLRKAYGEACS-----GPHCORHVCLRLQLTF 203
DB 148 TGADPVPVSAKSNHCLDAKACNLNDNCKLRSSYSISCNREISPTERCNRRKCHKALRQF 207

QY 204 FEKAAPHAQGLLCPAPNDRGCGERRNTIAPNCAL--PPVAPNCLERLRLCFSDPLCR 262
DB 208 FDRVPSYTYRMLFCSC--ODQACAEERRQTILPSCSYEDKEKPNCLDLRGVCRTHLCR 265

QY 263 SRLVDFQTHCHP--MDILGTCAEQSRCLRAYLGLIGTAMTNPVSNVNTSVALS--CTC 318
DB 266 SRLADPHANCRAASYQTVTSCPADNYQACLGSGVAGMIGFDMTPNYVDSSPTGIVVSPWCSC 325

QY 319 RGSGLNLOECEMLEGFFSHNPCLTEAIAA 347
DB 326 RGSNGNEECERFLRDFTEFNPCLRNAIOA 354

RESULT 14
Q6GTR9 HUMAN
ID Q6GTR9 HUMAN PRELIMINARY; PRT; 464 AA.
AC Q6GTR9;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DE GDNF family receptor alpha 2, preproprotein.
GN Name=GFPRA2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Tothiyuki S., Carninci P., Frange C.,
RA Raha S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny K.C., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
```

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RA Director MGC Project;
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC041688; AAH41688.1; -, mRNA.
KW Receptor.
SQ SEQUENCE 464 AA; 51543 MW; 8BC61529530FF21F CRC64;

Query Match 24.7%; Score 540.5; DB 2; Length 464;
Best Local Similarity 36.5%; Pred. No. 5.2e-35;
Matches 120; Conservative 47; Mismatches 123; Indels 39; Gaps 10;

QY 44 CLOARRKCOADPTCSAAVHLDSCYS--SISPLSEEPSVPADCLEAAQQLRNSSLIGC 101
DB 40 CVRANELCAESNCSRYRTLQCLAGDRDNTMLANKE-----COAALEVLQESPLYDC 93

QY 102 MCHRRMKNQVACLIDYWTVHRARSIGNYELDVSPYEDVTTSKPKWNLNLSKL----- 152
DB 94 RCKRGMKKELQCLQIYWSIHGLGTEGEFFYEASPYE--PVTSR-----LSDIFRLASIFSG 147

QY 153 -----NMLKPDSDLCIKFAMLCITLNDKDLRKAYGEACS-----GPHCORHVCLRLQLTF 203
DB 148 TGADPVPVSAKSNHCLDAKACNLNDNCKLRSSYSISCNREISPTERCNRRKCHKALRQF 207

QY 204 FEKAAPHAQGLLCPAPNDRGCGERRNTIAPNCAL--PPVAPNCLERLRLCFSDPLCR 262
DB 208 FDRVPSYTYRMLFCSC--ODQACAEERRQTILPSCSYEDKEKPNCLDLRGVCRTHLCR 265

QY 263 SRLVDFQTHCHP--MDILGTCAEQSRCLRAYLGLIGTAMTNPVSNVNTSVALS--CTC 318
DB 266 SRLADPHANCRAASYQTVTSCPADNYQACLGSGVAGMIGFDMTPNYVDSSPTGIVVSPWCSC 325

QY 319 RGSGLNLOECEMLEGFFSHNPCLTEAIAA 347
DB 326 RGSNGNEECERFLRDFTEFNPCLRNAIOA 354

RESULT 15
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ID QSRAD6 PONPY PRELIMINARY; PRT; 464 AA.
AC QSRAD6;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DE Hypothetical protein DKFZp459C0228.
GN Name=DKFZp459C0228;
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Pongo.
OX NCBI_TaxID=9600;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Cortex;
RG The German cDNA Consortium;
RA Bloecker H., Boecher M., Brandt P., Mewes H.W., Weil B., Amid C.,
RA Osanger A., Fobo G., Han M., Wiemann S.;
RA Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
RL EMBL; CR859081; CAH91274.1; -, mRNA.
DR GO; GO:0004872; F1 receptor activity; IEA.
DR InterPro; IPR003438; GDNF_receptor.
DR InterPro; IPR003504; GDNF_receptorA2.
DR Pfam; PF02351; GDNF; 1.
DR PRINTS; PR01318; GDNFRALPHA2.
DR PRINTS; PR01316; GDNFRECEPTOR.
KW Hypothetical protein.
SQ SEQUENCE 464 AA; 51560 MW; 46441C50299CCCCA CRC64;

Query Match 24.7%; Score 540.5; DB 2; Length 464;
Best Local Similarity 36.5%; Pred. No. 5.2e-35;
Matches 120; Conservative 47; Mismatches 123; Indels 39; Gaps 10;

QY 44 CLOARRKCOADPTCSAAVHLDSCYS--SISPLSEEPSVPADCLEAAQQLRNSSLIGC 101
DB 40 CVRANELCAESNCSRYRTLQCLAGDRDNTMLANKE-----COAALEVLQESPLYDC 93
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OM protein - protein search, using sw model

Run on: May 12, 2006, 02:12:04 ; Search time 19.5734 Seconds
(without alignments)
959.442 Million cell updates/sec

Title: US-10-668-936-21
Perfect score: 2190
Sequence: 1 MVRPLNRPPLPPVVLMLLL.....PWVPSLFSCTPLILLISLW 400

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 250354 seqs, 4694837 residues

Total number of hits satisfying chosen parameters: 250354

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA New:
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4: /SIDSS5/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
5: /SIDSS5/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
6: /SIDSS5/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
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11: /SIDSS5/ptodata/1/pubpaa/US11_NEW_PUB.pep1.*
12: /SIDSS5/ptodata/1/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1646.5	75.2	397	11	US-11-253-151-33
2	542.5	24.8	444	11	US-11-253-151-34
3	540.5	24.7	464	9	US-10-745-586-112
4	511	23.3	468	11	US-11-253-151-35
5	497.5	22.7	431	11	US-11-253-151-32
6	361	16.5	258	11	US-11-253-151-9
7	361	16.5	273	11	US-11-253-151-8
8	132	6.0	580	11	US-11-183-136-8
9	129	5.9	1057	11	US-11-149-003-6
10	129	5.9	1251	11	US-11-149-003-16
11	129	5.9	1342	11	US-11-149-003-24
12	129	5.9	1512	11	US-11-149-003-10
13	129	5.9	1570	11	US-11-149-003-12
14	129	5.9	1628	11	US-11-149-003-2
15	123.5	5.6	2871	11	US-11-169-041-131
16	123.5	5.6	3002	9	US-10-821-234-916
17	123	5.6	999	11	US-11-113-424-36
18	120	5.5	1170	11	US-11-114-962-5
19	119.5	5.5	997	11	US-11-113-424-37
20	117.5	5.4	508	9	US-10-915-160-2
21	116	5.3	3635	11	US-11-019-711-47

22	115	5.3	451	9	US-10-915-160-6	Sequence 6, Appli
23	114.5	5.2	470	9	US-10-915-160-4	Sequence 4, Appli
24	114	5.2	1433	11	US-11-114-962-1	Sequence 1, Appli
25	113.5	5.2	1192	11	US-11-149-003-18	Sequence 18, Appl
26	113.5	5.2	1207	11	US-11-149-003-20	Sequence 20, Appl
27	113.5	5.2	1477	11	US-11-149-003-8	Sequence 8, Appli
28	113.5	5.2	1535	11	US-11-149-003-14	Sequence 14, Appl
29	113.5	5.2	1566	9	US-10-453-372-1190	Sequence 1190, Ap
30	113.5	5.2	1593	11	US-11-149-003-4	Sequence 4, Appli
31	113.5	5.2	2026	8	US-10-505-928-831	Sequence 831, App
32	112.5	5.1	2556	11	US-11-050-346-67	Sequence 67, Appl
33	112	5.1	997	11	US-11-080-991-50	Sequence 50, Appl
34	111.5	5.1	434	11	US-11-241-956-5	Sequence 5, Appli
35	111.5	5.1	1609	11	US-11-072-175-185	Sequence 185, App
36	111	5.1	2440	9	US-10-766-317-10	Sequence 10, Appl
37	110	5.0	4544	9	US-10-501-035-214	Sequence 214, App
38	110	5.0	4544	11	US-11-076-427A-32	Sequence 32, Appl
39	109	5.0	580	11	US-11-183-136-6	Sequence 6, Appli
40	109	5.0	580	11	US-11-046-653-2	Sequence 2, Appli
41	109	5.0	2471	11	US-11-050-346-68	Sequence 68, Appl
42	108.5	5.0	1544	9	US-10-453-372-1186	Sequence 1186, Ap
43	108.5	5.0	1565	9	US-10-453-372-1180	Sequence 1180, Ap
44	108.5	5.0	2053	9	US-10-453-372-1174	Sequence 1174, Ap
45	108.5	5.0	2143	9	US-10-453-372-1188	Sequence 1188, Ap

ALIGNMENTS

RESULT 1
US-11-253-151-33
; Sequence 33, Application US/11253151
; Publication No. US20060069242A1
; GENERAL INFORMATION:
; APPLICANT: MASURE, STEFAN L.J.
; APPLICANT: CIK, MIROSLAV
; TITLE OF INVENTION: NEUROTROPIC FACTOR RECEPTOR
; FILE REFERENCE: JAB-1512
; CURRENT APPLICATION NUMBER: US/11/253,151
; PRIOR FILING DATE: 2005-10-18
; PRIOR APPLICATION NUMBER: PCT/EP00/04918
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 9915200.1
; PRIOR FILING DATE: 1999-06-29
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 33
; LENGTH: 397
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-253-151-33

Query Match	75.2%	Score	1646.5	DB 11	Length	397			
Best Local Similarity	77.8%	Pred. No.	2.1e-142						
Matches	305	Conservative	30	Mismatches	56	Indels	1	Gaps	1
Qy	9	PLPPVVLMLLLPPSPPLAAGDPLPTESRLMNSCLQARRKCOADPTCSAAVHLLDSC	68						
Db	7	PRPP-LMLLLVLSLPLGAGNSLATENRFVNSTQARKKCEANPACKAAVOHLSCT	65						
Qy	69	SSISTPLPSEEPSVPADCLEAAQQLRNSLIGCMCHRMKNQVACLDIYVTVHRAISLGN	128						
Db	66	SSLSRPLPLEESAMGADCLEAEQLNSLIDCRCHRMKHQATCLDIYVTVHPARSLGD	125						
Qy	129	YELDVSPYEDTVTSKPKWNLSKLNMLKPDSDICLKPFAMLCITLNDKCDRLRKAYGEACSG	188						
Db	126	YELDVSPYEDTVTSKPKWNLSKLNMLKPDSDICLKPFAMLCITLHDKCDRLRKAYGEACSG	185						
Qy	189	PHCORHVLQRLTLTFEKAAPHAQGLLLCPCAPNDRGCGERRRNTIAPNCALPPVPAPNC	248						
Db	186	IRCQRHLCAQLRSFFEKAASHAQGLLLCPCAPEDAGCGERRRNTIAPSCALPSVTPPNC	245						

QY 249 LELRLCFSDPLCRSLVDFQTHCHPMDILGTCAEQSRCLRAYLGLIGTAMTNPFSNV 308
 DB 246 LELRLCFSDPLCRSLVDFQTHCHPMDILGTCAEQSRCLRAYLGLIGTAMTNPFSKV 305
 QY 309 NTSVALSCTCRSGNLQECMELEGFSFNPCLTETAAAKMFHFSOLFQSDWPHPTFAVM 368
 DB 306 NTVVALSCTCRSGNLQECMELEGFSFNPCLTETAAAKMFHFSOLFQSDWADSTFSV 365
 QY 369 AHQNPENPAVRQPPWPSLFCSTLPLILLSLW 400
 DB 366 QQQNSNPALRQPLPILSILPLILLQTLW 397

RESULT 2

US-11-253-151-34
 ; Sequence 34, Application US/11253151
 ; Publication No. US20060069242A1
 ; GENERAL INFORMATION:
 ; APPLICANT: MASURE, STEFAN L.J.
 ; APPLICANT: CIK, MIROSLAV
 ; APPLICANT: HOEFNAGEL, EVERT W.
 ; TITLE OF INVENTION: NEUROTROPHIC FACTOR RECEPTOR
 ; FILE REFERENCE: JAB-1512
 ; CURRENT APPLICATION NUMBER: US/11/253,151
 ; CURRENT FILING DATE: 2005-10-18
 ; PRIOR APPLICATION NUMBER: PCT/EP00/04918
 ; PRIOR FILING DATE: 2000-05-26
 ; PRIOR APPLICATION NUMBER: GB 9915200.1
 ; PRIOR FILING DATE: 1999-06-29
 ; NUMBER OF SEQ ID NOS: 48
 ; SOFTWARE: Patent in Ver. 3.2
 ; SEQ ID NO 34
 ; LENGTH: 444
 ; TYPE: PRT
 ; ORGANISM: Rattus rattus
 ; US-11-253-151-34

Query Match 24.8%; Score 542.5; DB 11; Length 444;
 Best Local Similarity 37.4%; Pred. No. 1.2e-41;
 Matches 123; Conservative 42; Mismatches 125; Indels 39; Gaps 10;
 QY 44 CLOARRKCOADPTCSAAVHHLDSCTS--SISTPLPSEEPSVPADCLAAQQLRNSSLIGC 101
 DB 40 CVRANELCAAESNCSSRYRTLROCLAGRDNTMLANKE-----COAALEVLQESPLYDC 93
 QY 102 MCHRRMKNQVACLDIYTWTHRRARSLGNYELDVSPYEDTVTSPKWNLSKLNML-----155
 DB 94 RCKRGMKKELQCLQIYWSIHGLTEGEEFYEAAPYE--PVTSR-----LSDIFRLASIFSG 147
 QY 156 -----KPSDILCLKFMCLCTLNKCDRLRKAYGEACS-----GPHCQRHVCLRLTLTF 203
 DB 148 TGTDPAVSTKSNHCLDAAKACNLNDNCKLRSSYISICNREISPTERCNRRKCHKALRQF 207
 QY 204 FEKAEPHAQGLLLCPAPNDRCGERRRNTIAPNCAL--PPVAPNCLLELRRLCFSDPLCR 262
 DB 208 FDRVPSEYTYRMLFCSC--QDQACABRRRTILPSCSYEDKPKNCLDLRGVCTDHLCR 265
 QY 263 SRLVDFQTHCHP--MDILGTCAEQSRCLRAYLGLIGTAMTNPFSNVNVTVALS--CTC 318
 DB 266 SRLADFHANCRAASYRTITSCPADNYQACLSYAGMIGFDMTPNYVDSSTPTGIWVSPWCNC 325
 QY 319 RGSGLNQECEMLEGFPFSHPNCLTEAIAA 347
 DB 326 RGSGLNQECEKFLRDFTENPCLRNAIQA 354

RESULT 3

US-10-745-586-112
 ; Sequence 112, Application US/10745586
 ; Publication No. US20060063227A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Jacobs, Kenneth
 ; APPLICANT: McCoy, John M.

; APPLICANT: LaVallie, Edward R.
 ; APPLICANT: Collins-Racie, Lisa A.
 ; APPLICANT: Evans, Cheryl
 ; APPLICANT: Merbers, David
 ; APPLICANT: Treacy, Maurice
 ; APPLICANT: Bowman, Michael R.
 ; APPLICANT: Spaulding, Vikki
 ; APPLICANT: Agostino, Michael J.
 ; APPLICANT: Genetics Institute, Inc.
 ; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
 ; FILE REFERENCE: GI 6011-18X
 ; CURRENT APPLICATION NUMBER: US/10/745,586
 ; CURRENT FILING DATE: 2003-12-29
 ; PRIOR APPLICATION NUMBER: US/09/398,829
 ; PRIOR FILING DATE: 1999-09-17
 ; NUMBER OF SEQ ID NOS: 283
 ; SOFTWARE: Patent in Ver. 2.0
 ; SEQ ID NO 112
 ; LENGTH: 464
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-745-586-112

Query Match 24.7%; Score 540.5; DB 9; Length 464;
 Best Local Similarity 36.5%; Pred. No. 2e-41;
 Matches 120; Conservative 47; Mismatches 123; Indels 39; Gaps 10;
 QY 44 CLOARRKCOADPTCSAAVHHLDSCTS--SISTPLPSEEPSVPADCLAAQQLRNSSLIGC 101
 DB 40 CVRANELCAAESNCSSRYRTLROCLAGRDNTMLANKE-----COAALEVLQESPLYDC 93
 QY 102 MCHRRMKNQVACLDIYTWTHRRARSLGNYELDVSPYEDTVTSPKWNLSKLNML-----152
 DB 94 RCKRGMKKELQCLQIYWSIHGLTEGEEFYEAAPYE--PVTSR-----LSDIFRLASIFSG 147
 QY 153 ----NMLKPSDILCLKFMCLCTLNKCDRLRKAYGEACS-----GPHCQRHVCLRLTLTF 203
 DB 148 TGTDPVWSAKSNHCLDAAKACNLNDNCKLRSSYISICNREISPTERCNRRKCHKALRQF 207
 QY 204 FEKAEPHAQGLLLCPAPNDRCGERRRNTIAPNCAL--PPVAPNCLLELRRLCFSDPLCR 262
 DB 208 FDRVPSEYTYRMLFCSC--QDQACABRRRTILPSCSYEDKPKNCLDLRGVCTDHLCR 265
 QY 263 SRLVDFQTHCHP--MDILGTCAEQSRCLRAYLGLIGTAMTNPFSNVNVTVALS--CTC 318
 DB 266 SRLADFHANCRAASYQTVITSCPADNYQACLSYAGMIGFDMTPNYVDSSTPTGIWVSPWCSC 325
 QY 319 RGSGLNQECEMLEGFPFSHPNCLTEAIAA 347
 DB 326 RGSGLNQECEKFLRDFTENPCLRNAIQA 354

RESULT 4

US-11-253-151-35
 ; Sequence 35, Application US/11253151
 ; Publication No. US20060069242A1
 ; GENERAL INFORMATION:
 ; APPLICANT: MASURE, STEFAN L.J.
 ; APPLICANT: CIK, MIROSLAV
 ; APPLICANT: HOEFNAGEL, EVERT W.
 ; TITLE OF INVENTION: NEUROTROPHIC FACTOR RECEPTOR
 ; FILE REFERENCE: JAB-1512
 ; CURRENT APPLICATION NUMBER: US/11/253,151
 ; CURRENT FILING DATE: 2005-10-18
 ; PRIOR APPLICATION NUMBER: PCT/EP00/04918
 ; PRIOR FILING DATE: 2000-05-26
 ; PRIOR APPLICATION NUMBER: GB 9915200.1
 ; PRIOR FILING DATE: 1999-06-29
 ; NUMBER OF SEQ ID NOS: 48
 ; SOFTWARE: Patent in Ver. 3.2
 ; SEQ ID NO 35
 ; LENGTH: 468
 ; TYPE: PRT

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; ORGANISM: Rattus rattus
US-11-253-151-35

Query Match      23.3%; Score 511; DB 11; Length 468;
Best Local Similarity 36.0%; Pred. No. 9.7e-39;
Matches 130; Conservative 44; Mismatches 135; Indels 52; Gaps 13;

QY 17 LLLLLPSPPLAA-----GDPLPTESRLMNSCLQARKKQADPTCSAAAYHHLDSCTS--- 69
Db 17 LLLLLPSPPLAA-----GDPLPTESRLMNSCLQARKKQADPTCSAAAYHHLDSCTS--- 69
QY 70 ---SISTPLSEPSVPADCLAAQQLRNSLSLGCCHRRMKQVACLDIYVTHRARS 126
Db 70 ---SISTPLSEPSVPADCLAAQQLRNSLSLGCCHRRMKQVACLDIYVTHRARS 126
QY 58 TNFSLSLGLSAKO-----ECRSAMEALKOKSLYNCRCRKGKKEKNCRLIYWSYQSLQ- 111
Db 58 TNFSLSLGLSAKO-----ECRSAMEALKOKSLYNCRCRKGKKEKNCRLIYWSYQSLQ- 111
QY 127 GNYELDVSPYEDVTWTSKPMKMLSKLMLKP-DSDL-----CLKFAMLCPLND 173
Db 127 GNYELDVSPYEDVTWTSKPMKMLSKLMLKP-DSDL-----CLKFAMLCPLND 173
QY 112 GNDLLEDSPE-----PVNSRLSDIFRAVPFISDVFEQVQVHEHISKGNCLDAKACMLDD 165
Db 112 GNDLLEDSPE-----PVNSRLSDIFRAVPFISDVFEQVQVHEHISKGNCLDAKACMLDD 165
QY 174 KCDRLKAYGEAC-----SGPHCQHVCLRLQLLTFFKAAEPHAQGLLALCPAPNDRGCGE 229
Db 174 KCDRLKAYGEAC-----SGPHCQHVCLRLQLLTFFKAAEPHAQGLLALCPAPNDRGCGE 229
QY 166 TCKYRSAYITPCTTSMSNEVCNRRKCHKALRQFFDKVPAKHSYGLFCSC--RDIACTE 223
Db 166 TCKYRSAYITPCTTSMSNEVCNRRKCHKALRQFFDKVPAKHSYGLFCSC--RDIACTE 223
QY 230 RRENTIAPCALPP-VAPNCLERLRLCFSDPLCRSLRVDFTQCHPMD--ILGTCATEQ-S 286
Db 230 RRENTIAPCALPP-VAPNCLERLRLCFSDPLCRSLRVDFTQCHPMD--ILGTCATEQ-S 286
QY 224 RROTIVPVCSYEERENPCLSLQDSCKTYIICRSLADFTTNCQPESSVSNCLKENYA 283
Db 224 RROTIVPVCSYEERENPCLSLQDSCKTYIICRSLADFTTNCQPESSVSNCLKENYA 283
QY 287 RCLRAYLGLGTAMTNPVSNVNTSVALSCTCRGSGNLQECMELEGFFSHNPLCTEIA 346
Db 287 RCLRAYLGLGTAMTNPVSNVNTSVALSCTCRGSGNLQECMELEGFFSHNPLCTEIA 346
QY 284 DCLLAYSGLLGTWTPNYVDSSLSVAPWCDSCNSGNDLEDCLKFLNFFKDNLTCLKNAIQ 343
Db 284 DCLLAYSGLLGTWTPNYVDSSLSVAPWCDSCNSGNDLEDCLKFLNFFKDNLTCLKNAIQ 343
QY 347 A 347
Db 347 A 347
QY 344 A 344
Db 344 A 344

RESULT 5
US-11-253-151-32
; Sequence 32, Application US/11253151
; Publication No. US2006069242A1
; GENERAL INFORMATION:
; APPLICANT: MASURE, STEFAN L.J.
; APPLICANT: CIK, MIROSLAV
; TITLE OF INVENTION: NEUROTROPHIC FACTOR RECEPTOR
; FILE REFERENCE: JAB-1512
; CURRENT APPLICATION NUMBER: US/11/253,151
; PRIOR FILING DATE: 2005-10-18
; PRIOR APPLICATION NUMBER: PCT/EP00/04918
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 9915200.1
; PRIOR FILING DATE: 1999-06-29
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 32
; LENGTH: 431
; TYPE: PRT
; ORGANISM: Gallus gallus
US-11-253-151-32

Query Match      22.7%; Score 497.5; DB 11; Length 431;
Best Local Similarity 34.8%; Pred. No. 1.5e-37;
Matches 111; Conservative 37; Mismatches 148; Indels 23; Gaps 8;

QY 44 CLOARKKQADPTCSAAAYHHLDSCTSSISTPLSEPSVPADCLAAQQLRNSLSLGCWC 103
Db 44 CLOARKKQADPTCSAAAYHHLDSCTSSISTPLSEPSVPADCLAAQQLRNSLSLGCWC 103
QY 26 CLOAGSCTNDPTCSSKFTLRQCIA--GNGAKLGDPAKQCRSTVTALLSSQLYGCK 83
Db 26 CLOAGSCTNDPTCSSKFTLRQCIA--GNGAKLGDPAKQCRSTVTALLSSQLYGCK 83
QY 104 HRMKQVACLDIYVTHRARSIGNVELDVSPYEDVTWTSKPMKMLSKLMLKPDS--- 160
Db 104 HRMKQVACLDIYVTHRARSIGNVELDVSPYEDVTWTSKPMKMLSKLMLKPDS--- 160
QY 84 KGMKKEKCLSVYSIHITLMGMVLESSPYEPFIRG-----FDVRLASTAGSENV 139
Db 84 KGMKKEKCLSVYSIHITLMGMVLESSPYEPFIRG-----FDVRLASTAGSENV 139
QY 161 ----LCLKFAMLCPLNDKCDRLKAYGEAC-----SGPHCQHVCLRLQLLTFFKAAEPH 211
Db 161 ----LCLKFAMLCPLNDKCDRLKAYGEAC-----SGPHCQHVCLRLQLLTFFKAAEPH 211

; ORGANISM: Rattus rattus
US-11-253-151-35

Query Match      23.3%; Score 511; DB 11; Length 468;
Best Local Similarity 36.0%; Pred. No. 9.7e-39;
Matches 130; Conservative 44; Mismatches 135; Indels 52; Gaps 13;

QY 17 LLLLLPSPPLAA-----GDPLPTESRLMNSCLQARKKQADPTCSAAAYHHLDSCTS--- 69
Db 17 LLLLLPSPPLAA-----GDPLPTESRLMNSCLQARKKQADPTCSAAAYHHLDSCTS--- 69
QY 70 ---SISTPLSEPSVPADCLAAQQLRNSLSLGCCHRRMKQVACLDIYVTHRARS 126
Db 70 ---SISTPLSEPSVPADCLAAQQLRNSLSLGCCHRRMKQVACLDIYVTHRARS 126
QY 58 TNFSLSLGLSAKO-----ECRSAMEALKOKSLYNCRCRKGKKEKNCRLIYWSYQSLQ- 111
Db 58 TNFSLSLGLSAKO-----ECRSAMEALKOKSLYNCRCRKGKKEKNCRLIYWSYQSLQ- 111
QY 127 GNYELDVSPYEDVTWTSKPMKMLSKLMLKP-DSDL-----CLKFAMLCPLND 173
Db 127 GNYELDVSPYEDVTWTSKPMKMLSKLMLKP-DSDL-----CLKFAMLCPLND 173
QY 112 GNDLLEDSPE-----PVNSRLSDIFRAVPFISDVFEQVQVHEHISKGNCLDAKACMLDD 165
Db 112 GNDLLEDSPE-----PVNSRLSDIFRAVPFISDVFEQVQVHEHISKGNCLDAKACMLDD 165
QY 174 KCDRLKAYGEAC-----SGPHCQHVCLRLQLLTFFKAAEPHAQGLLALCPAPNDRGCGE 229
Db 174 KCDRLKAYGEAC-----SGPHCQHVCLRLQLLTFFKAAEPHAQGLLALCPAPNDRGCGE 229
QY 166 TCKYRSAYITPCTTSMSNEVCNRRKCHKALRQFFDKVPAKHSYGLFCSC--RDIACTE 223
Db 166 TCKYRSAYITPCTTSMSNEVCNRRKCHKALRQFFDKVPAKHSYGLFCSC--RDIACTE 223
QY 230 RRENTIAPCALPP-VAPNCLERLRLCFSDPLCRSLRVDFTQCHPMD--ILGTCATEQ-S 286
Db 230 RRENTIAPCALPP-VAPNCLERLRLCFSDPLCRSLRVDFTQCHPMD--ILGTCATEQ-S 286
QY 224 RROTIVPVCSYEERENPCLSLQDSCKTYIICRSLADFTTNCQPESSVSNCLKENYA 283
Db 224 RROTIVPVCSYEERENPCLSLQDSCKTYIICRSLADFTTNCQPESSVSNCLKENYA 283
QY 287 RCLRAYLGLGTAMTNPVSNVNTSVALSCTCRGSGNLQECMELEGFFSHNPLCTEIA 346
Db 287 RCLRAYLGLGTAMTNPVSNVNTSVALSCTCRGSGNLQECMELEGFFSHNPLCTEIA 346
QY 284 DCLLAYSGLLGTWTPNYVDSSLSVAPWCDSCNSGNDLEDCLKFLNFFKDNLTCLKNAIQ 343
Db 284 DCLLAYSGLLGTWTPNYVDSSLSVAPWCDSCNSGNDLEDCLKFLNFFKDNLTCLKNAIQ 343
QY 347 A 347
Db 347 A 347
QY 344 A 344
Db 344 A 344

RESULT 6
US-11-253-151-9
; Sequence 9, Application US/11253151
; Publication No. US2006069242A1
; GENERAL INFORMATION:
; APPLICANT: MASURE, STEFAN L.J.
; APPLICANT: CIK, MIROSLAV
; TITLE OF INVENTION: NEUROTROPHIC FACTOR RECEPTOR
; FILE REFERENCE: JAB-1512
; CURRENT APPLICATION NUMBER: US/11/253,151
; CURRENT FILING DATE: 2005-10-18
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: PCT/EP00/04918
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 9915200.1
; PRIOR FILING DATE: 1999-06-29
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 9
; LENGTH: 258
; TYPE: PRT
; ORGANISM: Rattus rattus
US-11-253-151-9

Query Match      16.5%; Score 361; DB 11; Length 258;
Best Local Similarity 34.3%; Pred. No. 2.3e-25;
Matches 87; Conservative 25; Mismatches 102; Indels 40; Gaps 8;

QY 145 WKWNLKLANMLKPDSDCLCKLKFAMLCPLNDKCDRLKAYGEACSG-----PHCQHVCL 197
Db 145 WKWNLKLANMLKPDSDCLCKLKFAMLCPLNDKCDRLKAYGEACSG-----PHCQHVCL 197
QY 20 WSLGCGSGSASSTEGNRCVAAEAECTADECCQQLRSEYVAQCLGRAGWPGSCVSRRCR 79
Db 20 WSLGCGSGSASSTEGNRCVAAEAECTADECCQQLRSEYVAQCLGRAGWPGSCVSRRCR 79
QY 198 ROLLTFEKAEPHAQGLLALCPAPNDRGCGERRNTIAPNCAL--PPVA-PNCLERLRL 254
Db 198 ROLLTFEKAEPHAQGLLALCPAPNDRGCGERRNTIAPNCAL--PPVA-PNCLERLRL 254
QY 80 RALRREFPARGPPALTHALLFCGC--BGPACERRRQTFAFACAFSGPQLAPPSCLKPLDR 137
Db 80 RALRREFPARGPPALTHALLFCGC--BGPACERRRQTFAFACAFSGPQLAPPSCLKPLDR 137
QY 255 CFSDDLCSRLVDFQTHCHPMDILGT---CATEQS--RCLRAYLGLGTAMTNPVSNVNT 310
Db 255 CFSDDLCSRLVDFQTHCHPMDILGT---CATEQS--RCLRAYLGLGTAMTNPVSNVNT 310
QY 138 CERSRRCRPRLFAFQASCAPAP--GSRDGCPEGGPRCLRAYAGLVGTVTNYLNVSA 195
Db 138 CERSRRCRPRLFAFQASCAPAP--GSRDGCPEGGPRCLRAYAGLVGTVTNYLNVSA 195
QY 311 SVALSCTCRGSGNLQECMELEGFFSHNPLCTEIAAKMRHFSQLFSQDWPHTFAVMAH 370
Db 311 SVALSCTCRGSGNLQECMELEGFFSHNPLCTEIAAKMRHFSQLFSQDWPHTFAVMAH 370
QY 196 RVAPWCGCEASGNRRECEAFKLFTRNPLDGA1-----QAF 233
Db 196 RVAPWCGCEASGNRRECEAFKLFTRNPLDGA1-----QAF 233
QY 371 QNENPAVRPQPWVP 384
Db 371 QNENPAVRPQPWVP 384
QY 234 DSSQPSVLQDQWNP 247
Db 234 DSSQPSVLQDQWNP 247

RESULT 7
US-11-253-151-8
; Sequence 8, Application US/11253151
; Publication No. US2006069242A1
; GENERAL INFORMATION:
; APPLICANT: MASURE, STEFAN L.J.
; APPLICANT: CIK, MIROSLAV
; APPLICANT: HOEFNAGEL, EVERT W.
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; TITLE OF INVENTION: NEUROTROPHIC FACTOR RECEPTOR
; FILE REFERENCE: JAB-1512
; CURRENT APPLICATION NUMBER: US/11/253,151
; CURRENT FILING DATE: 2005-10-18
; PRIOR APPLICATION NUMBER: PCT/EP00/04918
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 9915200.1
; PRIOR FILING DATE: 1999-06-29
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 8
; LENGTH: 273
; TYPE: PRT
; ORGANISM: Rattus rattus
US-11-253-151-8

Query Match 16.5%; Score 361; DB 11; Length 273;
Best Local Similarity 34.3%; Pred. No. 2.5e-25;
Matches 87; Conservative 25; Mismatches 102; Indels 40; Gaps 8;

QY 145 WKNNLSKLNMLKPDSDLCIKFAMLTCLNDKCDRLRKAYGEACSG-----PHCORHVCL 197
Db 20 NSLGCQSGSASSTEGNRCVVEAAEACTADQCQQLRSEYVAQCLGRAGWPGSCVRSRCR 79

QY 198 ROLLTFEKAAPHAQGLLLCPACNDRCGGERRRNTIAPNCAL--PPVA-PNCLELRRL 254
Db 80 RALRRFFARGPPALTHALLFCGC--EGPACAEERRRQTAPACAFSGPQLAPPSCILKPLDR 137

QY 255 CFSDDLRSRLVDQTHCHPMILGT---CATEQS-RCRLAYLGLIGTAMTNPVSNVT 310
Db 138 CERSRRCRLPFAQASCAPAP--GSRDGCPEGGPRCLRAYAGLVGTVTNYLDNVA 195

QY 311 SVALSCTCRSGNLOCEMBLGGFTSHNPCLTEAIAAKMRFHSQLSQDFWPHPTFAVMAH 370
Db 196 RVAPWCGCEASGNRECEAFKIFTRNCLDGA-----QAF 233

QY 371 QNENPAVRQPWPV 384
Db 234 DSSQPSVLQDQNP 247

RESULT 8
US-11-183-136-8
; Sequence 8, Application US/11/183136
; Publication No. US20060019896A1
; GENERAL INFORMATION:
; APPLICANT: Li, Dean
; APPLICANT: Park, Kye Won
; TITLE OF INVENTION: NETRIN-RELATED COMPOSITIONS AND USES
; FILE REFERENCE: UUTH-P01-011
; CURRENT APPLICATION NUMBER: US/11/183,136
; CURRENT FILING DATE: 2005-07-14
; PRIOR APPLICATION NUMBER: US 60/587,796
; PRIOR FILING DATE: 2004-07-14
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 580
; TYPE: PRT
; ORGANISM: Mouse
US-11-183-136-8

Query Match 6.0%; Score 132; DB 11; Length 580;
Best Local Similarity 22.5%; Pred. No. 0.00047;
Matches 104; Conservative 40; Mismatches 194; Indels 124; Gaps 23;

QY 20 LLPSPPLPAAAGDPLPTESRLMNSCLQARKKCOADPTCSAAYHLD-----S 66
Db 97 LQAQAPFNVTLPVGLKAFELVFVSL---RFSAPPTSVALLKSDHGRSWVPLGFSSS 153

QY 67 CTSSIS-TPLPSEPSVP---ADCLEAAQ-----QLRNSSLIGC 101
Db 154 CTLDYGLPAPADGPGSGFEALCFPAPQAPDGGGLLAFVSQDGGSPQGLDLDNSPV--- 210

; TITLE OF INVENTION: NOVEL HUMAN KIEIN-LIKE PROTEINS AND POLYNUCLEOTIDES ENCODING THE
; SEQUENCE 6, APPLICATION US/11/149,003
; PUBLICATION NO. US20060014277A1
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Scoville, John
; TITLE OF INVENTION: NOVEL HUMAN KIEIN-LIKE PROTEINS AND POLYNUCLEOTIDES ENCODING THE
; TITLE OF INVENTION: SAME
; FILE REFERENCE: LEX-0360-USA
; CURRENT APPLICATION NUMBER: US/11/149,003
; CURRENT FILING DATE: 2005-06-09
; PRIOR APPLICATION NUMBER: US/10/189,971
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 60/302,949
; PRIOR FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: US 60/315,634
; PRIOR FILING DATE: 2001-08-29
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 1057
; TYPE: PRT
; ORGANISM: homo sapiens
US-11-149-003-6

Query Match 5.9%; Score 129; DB 11; Length 1057;
Best Local Similarity 20.6%; Pred. No. 0.0018;
Matches 92; Conservative 40; Mismatches 185; Indels 130; Gaps 25;

QY 33 PLPTESRLMNSCLQ-----ARRKQAD-----PTCSAAYHLDSCSSISSTP 74
Db 223 PDPREPNCILCTLGGFVTCTGRRPCBPBGSGHPLIPSGHCHCCPTCQGRYHGVTTASGETLP 282

QY 75 LPSEBSPVPADCLEAAQQLRNSSLIGCMCHRRMKNOVACLIDYIYTVHRRARSLGNLYELDVS 134
Db 283 DPLDPTCSILCTQEGSMRCKKFCAPALCPHSPGFCFP----VCHSCLSQGREQHODGE 338

QY 135 PYEDVTVTSKPM-KMNLKLNMLKPDSDLCIKF---AMLCTL-----NDKCDRLR--KAYG 183
Db 339 EFEGPAGSCWCRCAQAGVQS-----CVRLQCPPLPKLQVTERGSCPCRRCGLAHG 390

QY 184 E-----ACSGPHCQRHVCLRLQLLTFEKAAPHAQGLLCP--CAPNDRGCG 228
Db 391 EEHPESGRWVPDPSACSSCVCHGVVTCARIQICISSAQPR-QG-----PHDCCPQCSDC- 444
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Qy 229 ERRNTIAPNCALPPVAPNCLLELRCLFSDP-----LCRSRLVDFQTHCHPMDIL-- 278
Db 445 EHEGRKYEPGESFQFGADPC-----EVCICEPQEGPPLRCHRRQCPSLVGCPPSOLLPP 500
Qy 279 -----GTCATEQRCLRAYLGLIGTAMTNFVSNVNTSVALSCTCRGSGNL-----Q 325
Db 501 GPOHCCPTCAEALNSCSE---GLLGSELAP-----PDCYTCQCQDLTWLCTHQACPE 550
Qy 326 ECEMLEGFFSHNP-----CLTEATAAKMRHFSQLFSQDWPHTFAVMA----- 369
Db 551 LSCPLSE---RHTPPGSCCPVCRECVVEAEGRRV-----ADGESWRDPSNACIACHTCHRG 602
Qy 370 -----HONENPAVR--POPW--VPSLFSC 389
Db 603 HVECHLEEQALSCPHGWAKVPOADSC 629

RESULT 10
US-11-149-003-16
; Sequence 16, Application US/11149003
; Publication No. US20060014277A1
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: Novel Human Kielin-like Proteins and Polynucleotides Encoding the
; TITLE OF INVENTION: Same
; FILE REFERENCE: LEX-0360-USA
; CURRENT APPLICATION NUMBER: US/11/149,003
; PRIOR FILING DATE: 2005-06-09
; PRIOR APPLICATION NUMBER: US/10/189,971
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 60/302,949
; PRIOR FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: US 60/315,634
; PRIOR FILING DATE: 2001-08-29
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 1251
; TYPE: PRT
; ORGANISM: homo sapiens
US-11-149-003-16

Query Match 5.9%; Score 129; DB 11; Length 1251;
Best Local Similarity 20.6%; Pred. No. 0.0022;
Matches 92; Conservative 40; Mismatches 185; Indels 130; Gaps 25;

Qy 33 PLPTESRLMNSCLQ-----ARRKQAD-----PTCSAAYHHLDSCSSISTP 74
Db 417 PDPREPCNLCTCLGGFVTCGRRCPEPPGCGSHPLIPSGHCCTCGCRYHGVTTASGETLP 476
Qy 75 LPSEEPSVPADCLEAAQQLNSSLIGCMCHRRMKNQVACLDIYTVHRAARSLGNYELDVS 134
Db 477 DPLDPTCSLCTCQEGSMRCQKPCAPALCPHPSPGCFP-----VCHSCLSQGREHODGE 532
Qy 135 PYEDTVTSKPW--KXNLSKLANMLKPDSDLCLKF---AMLCTL-----NDKCDRLR--KAYG 183
Db 533 EFGPGAGSCWCRCQAGQVS-----CVRLQCPPLPCKLQVTERGSCCPRCRGCLAHG 584
Qy 184 E-----ACSGPHCORHVCLRLQLTTFEKAABPHAOGLLLCP--CAPNDRGCG 228
Db 585 EEHPGSRWVPPDSACSSCVCHGVVTCARIQCISSCAQPR-QG-----PHDCCPQCSDC- 638
Qy 229 ERRNTIAPNCALPPVAPNCLLELRCLFSDP-----LCRSRLVDFQTHCHPMDIL-- 278
Db 639 EHEGRKYEPGESFQFGADPC-----EVCICEPQEGPPLRCHRRQCPSLVGCPPSOLLPP 694
Qy 279 -----GTCATEQRCLRAYLGLIGTAMTNFVSNVNTSVALSCTCRGSGNL-----Q 325
Db 695 GPOHCCPTCAEALNSCSE---GLLGSELAP-----PDCYTCQCQDLTWLCTHQACPE 744
Qy 326 ECEMLEGFFSHNP-----CLTEATAAKMRHFSQLFSQDWPHTFAVMA----- 369
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Db 745 LSCPLSE---RHTPPGSCCPVCRECVVEAEGRRV-----ADGESWRDPSNACIACHTCHRG 796
Qy 370 -----HONENPAVR--POPW--VPSLFSC 389
Db 797 HVECHLEEQALSCPHGWAKVPOADSC 823

RESULT 11
US-11-149-003-24
; Sequence 24, Application US/11149003
; Publication No. US20060014277A1
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: Novel Human Kielin-like Proteins and Polynucleotides Encoding th
; TITLE OF INVENTION: Same
; FILE REFERENCE: LEX-0360-USA
; CURRENT APPLICATION NUMBER: US/11/149,003
; CURRENT FILING DATE: 2005-06-09
; PRIOR APPLICATION NUMBER: US/10/189,971
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 60/302,949
; PRIOR FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: US 60/315,634
; PRIOR FILING DATE: 2001-08-29
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 1342
; TYPE: PRT
; ORGANISM: homo sapiens
US-11-149-003-24

Query Match 5.9%; Score 129; DB 11; Length 1342;
Best Local Similarity 20.6%; Pred. No. 0.0024;
Matches 92; Conservative 40; Mismatches 185; Indels 130; Gaps 25;

Qy 33 PLPTESRLMNSCLQ-----ARRKQAD-----PTCSAAYHHLDSCSSISTP 74
Db 508 PDPREPCNLCTCLGGFVTCGRRCPEPPGCGSHPLIPSGHCCTCGCRYHGVTTASGETLP 567
Qy 75 LPSEEPSVPADCLEAAQQLNSSLIGCMCHRRMKNQVACLDIYTVHRAARSLGNYELDVS 134
Db 568 DPLDPTCSLCTCQEGSMRCQKPCAPALCPHPSPGCFP-----VCHSCLSQGREHODGE 623
Qy 135 PYEDTVTSKPW--KXNLSKLANMLKPDSDLCLKF---AMLCTL-----NDKCDRLR--KAYG 183
Db 624 EFGPGAGSCWCRCQAGQVS-----CVRLQCPPLPCKLQVTERGSCCPRCRGCLAHG 675
Qy 184 E-----ACSGPHCORHVCLRLQLTTFEKAABPHAOGLLLCP--CAPNDRGCG 228
Db 676 EEHPGSRWVPPDSACSSCVCHGVVTCARIQCISSCAQPR-QG-----PHDCCPQCSDC- 729
Qy 229 ERRNTIAPNCALPPVAPNCLLELRCLFSDP-----LCRSRLVDFQTHCHPMDIL-- 278
Db 730 EHEGRKYEPGESFQFGADPC-----EVCICEPQEGPPLRCHRRQCPSLVGCPPSOLLPP 785
Qy 279 -----GTCATEQRCLRAYLGLIGTAMTNFVSNVNTSVALSCTCRGSGNL-----Q 325
Db 786 GPOHCCPTCAEALNSCSE---GLLGSELAP-----PDCYTCQCQDLTWLCTHQACPE 835
Qy 326 ECEMLEGFFSHNP-----CLTEATAAKMRHFSQLFSQDWPHTFAVMA----- 369
Db 836 LSCPLSE---RHTPPGSCCPVCRECVVEAEGRRV-----ADGESWRDPSNACIACHTCHRG 887
Qy 370 -----HONENPAVR--POPW--VPSLFSC 389
Db 888 HVECHLEEQALSCPHGWAKVPOADSC 914

RESULT 12
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US-11-149-003-10
; Sequence 10, Application US/11149003
; Publication No. US20060014277A1
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: Novel Human Kiellin-like Proteins and Polynucleotides Encoding the
; FILE REFERENCE: LEX-0360-USA
; CURRENT APPLICATION NUMBER: US/11/149,003
; CURRENT FILING DATE: 2005-06-09
; PRIOR APPLICATION NUMBER: US/10/189,971
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 60/302,949
; PRIOR FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: US 60/315,634
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 1512
; TYPE: PRT
; ORGANISM: homo sapiens
; ORGANISM: Same
US-11-149-003-10

Query Match          5.9%; Score 129; DB 11; Length 1512;
Best Local Similarity 20.6%; Pred. No. 0.0028;
Matches 92; Conservative 40; Mismatches 185; Indels 130; Gaps 25;

QY 33 PLPTESRLMNSCLQ-----ARRKQAD-----PTCSAAVHLDSTCTSSISTP 74
      |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db 678 PDREPCNLCTCLGGFVTCGRRCPPGCSHPLIPSGHCCPTCQGCRCYHGVTTASGETLP 737
      |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :

QY 75 LPSEEPSVPADCLEAAQQLRNSLLIGCMCHRRMKNQVACLDIYVTVHRRARSLGNYELDVS 134
      |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db 738 DPLDPTCSLCTCQEGSMRCQKPCAPALCPHPSPGFCFP-----VCHSCLSQGREHODGE 793
      |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :

QY 135 PYEDVTVTSKPM-KMNLKSLKMLKPDSDLCLKF---AMLCTL-----NDKCDRLR--KAYG 183
      |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db 794 ELEGPGAGSCWCRCQAGQVS-----CVRLQCPPLPCKLVTERGSCCPRCRCGLAHG 845
      |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :

QY 184 E-----ACSGPHCQRHVCLRQLLTFFEKAAEPHAGQLLLCP--CAPNDRGCG 228
      |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db 846 EEHPEGSRWVPPDSACSCVCHGVVTCARIQICISSCAQPR-QG-----PHDCCPQCSDC- 899
      |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :

QY 229 ERRRNTIAPNCALPPVAPNCLERLRCFSDP-----LCRSRLVDFQTHCHPMDL-- 278
      |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db 900 EHEGRKYEPGESFPQADPC---EVCICEPQEGPPSLRCHRRQCPSLVGCPSPQLLPP 955
      |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :

QY 279 -----GTCATEQSRCLRAYLGLIGTAMTFNFVSNVNTSVALSCTCGSGNL-----Q 325
      |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db 956 GPQHCCPTCAEALNSCSE---GLLGSELAP-----PDPCYTCQCQDLTWLCIHQACPE 1005
      |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :

QY 326 EECEMLEGFPFSHPN-----CLTEAIAAKMRHFSQLFSQDWPHPTFAVMA----- 369
      |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db 1006 LSCPLSE---RHPTPGSCCPVCRECVVEAEGRRV-----ADGESWRDPFNACIACHTCHRG 1057
      |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :

QY 370 ----HQENPAVR-POPW--VPSLFSC 389
      |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db 1058 HVECHLEECQALSCPHGMAKVPQADSC 1084
      |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :

RESULT 13
US-11-149-003-12
; Sequence 12, Application US/11149003
; Publication No. US20060014277A1
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: Novel Human Kiellin-like Proteins and Polynucleotides Encoding the
; FILE REFERENCE: LEX-0360-USA
; CURRENT APPLICATION NUMBER: US/11/149,003
; CURRENT FILING DATE: 2005-06-09
; PRIOR APPLICATION NUMBER: US/10/189,971
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 60/302,949
; PRIOR FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: US 60/315,634
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 1570
; TYPE: PRT
; ORGANISM: homo sapiens
; ORGANISM: Same
US-11-149-003-12

Query Match          5.9%; Score 129; DB 11; Length 1570;
Best Local Similarity 20.6%; Pred. No. 0.0029;
Matches 92; Conservative 40; Mismatches 185; Indels 130; Gaps 25;

QY 33 PLPTESRLMNSCLQ-----ARRKQAD-----PTCSAAVHLDSTCTSSISTP 74
      |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db 736 PDREPCNLCTCLGGFVTCGRRCPPGCSHPLIPSGHCCPTCQGCRCYHGVTTASGETLP 795
      |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :

QY 75 LPSEEPSVPADCLEAAQQLRNSLLIGCMCHRRMKNQVACLDIYVTVHRRARSLGNYELDVS 134
      |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db 796 DPLDPTCSLCTCQEGSMRCQKPCAPALCPHPSPGFCFP-----VCHSCLSQGREHODGE 851
      |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :

QY 135 PYEDVTVTSKPM-KMNLKSLKMLKPDSDLCLKF---AMLCTL-----NDKCDRLR--KAYG 183
      |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db 852 ELEGPGAGSCWCRCQAGQVS-----CVRLQCPPLPCKLVTERGSCCPRCRCGLAHG 903
      |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :

QY 184 E-----ACSGPHCQRHVCLRQLLTFFEKAAEPHAGQLLLCP--CAPNDRGCG 228
      |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db 904 EEHPEGSRWVPPDSACSCVCHGVVTCARIQICISSCAQPR-QG-----PHDCCPQCSDC- 957
      |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :

QY 229 ERRRNTIAPNCALPPVAPNCLERLRCFSDP-----LCRSRLVDFQTHCHPMDL-- 278
      |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db 958 EHEGRKYEPGESFPQADPC---EVCICEPQEGPPSLRCHRRQCPSLVGCPSPQLLPP 1013
      |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :

QY 279 -----GTCATEQSRCLRAYLGLIGTAMTFNFVSNVNTSVALSCTCGSGNL-----Q 325
      |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db 1014 GPQHCCPTCAEALNSCSE---GLLGSELAP-----PDPCYTCQCQDLTWLCIHQACPE 1063
      |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :

QY 326 EECEMLEGFPFSHPN-----CLTEAIAAKMRHFSQLFSQDWPHPTFAVMA----- 369
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Db 1064 LSCPLSE---RHPTPGSCCPVCRECVVEAEGRRV-----ADGESWRDPFNACIACHTCHRG 1115
      |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :

QY 370 ----HQENPAVR-POPW--VPSLFSC 389
      |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db 1116 HVECHLEECQALSCPHGMAKVPQADSC 1142
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RESULT 14
US-11-149-003-2
; Sequence 2, Application US/11149003
; Publication No. US20060014277A1
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: Novel Human Kiellin-like Proteins and Polynucleotides Encoding the
; FILE REFERENCE: LEX-0360-USA
; CURRENT APPLICATION NUMBER: US/11/149,003
; CURRENT FILING DATE: 2005-06-09
; PRIOR APPLICATION NUMBER: US/10/189,971
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 60/302,949
; PRIOR FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: US 60/315,634
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 1570
; TYPE: PRT
; ORGANISM: homo sapiens
; ORGANISM: Same
US-11-149-003-12
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US-11-149-003-10
; Sequence 10, Application US/11149003
; Publication No. US20060014277A1
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: Novel Human Kiellin-like Proteins and Polynucleotides Encoding the
; FILE REFERENCE: LEX-0360-USA
; CURRENT APPLICATION NUMBER: US/11/149,003
; CURRENT FILING DATE: 2005-06-09
; PRIOR APPLICATION NUMBER: US/10/189,971
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 60/302,949
; PRIOR FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: US 60/315,634
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 1570
; TYPE: PRT
; ORGANISM: homo sapiens
; ORGANISM: Same
US-11-149-003-12

Query Match          5.9%; Score 129; DB 11; Length 1570;
Best Local Similarity 20.6%; Pred. No. 0.0029;
Matches 92; Conservative 40; Mismatches 185; Indels 130; Gaps 25;

QY 33 PLPTESRLMNSCLQ-----ARRKQAD-----PTCSAAVHLDSTCTSSISTP 74
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Db 736 PDREPCNLCTCLGGFVTCGRRCPPGCSHPLIPSGHCCPTCQGCRCYHGVTTASGETLP 795
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QY 75 LPSEEPSVPADCLEAAQQLRNSLLIGCMCHRRMKNQVACLDIYVTVHRRARSLGNYELDVS 134
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Db 796 DPLDPTCSLCTCQEGSMRCQKPCAPALCPHPSPGFCFP-----VCHSCLSQGREHODGE 851
      |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :

QY 135 PYEDVTVTSKPM-KMNLKSLKMLKPDSDLCLKF---AMLCTL-----NDKCDRLR--KAYG 183
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Db 852 ELEGPGAGSCWCRCQAGQVS-----CVRLQCPPLPCKLVTERGSCCPRCRCGLAHG 903
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QY 184 E-----ACSGPHCQRHVCLRQLLTFFEKAAEPHAGQLLLCP--CAPNDRGCG 228
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Db 904 EEHPEGSRWVPPDSACSCVCHGVVTCARIQICISSCAQPR-QG-----PHDCCPQCSDC- 957
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QY 229 ERRRNTIAPNCALPPVAPNCLERLRCFSDP-----LCRSRLVDFQTHCHPMDL-- 278
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Db 958 EHEGRKYEPGESFPQADPC---EVCICEPQEGPPSLRCHRRQCPSLVGCPSPQLLPP 1013
      |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :

QY 279 -----GTCATEQSRCLRAYLGLIGTAMTFNFVSNVNTSVALSCTCGSGNL-----Q 325
      |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db 1014 GPQHCCPTCAEALNSCSE---GLLGSELAP-----PDPCYTCQCQDLTWLCIHQACPE 1063
      |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :

QY 326 EECEMLEGFPFSHPN-----CLTEAIAAKMRHFSQLFSQDWPHPTFAVMA----- 369
      |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
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QY 370 ----HQENPAVR-POPW--VPSLFSC 389
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Db 1116 HVECHLEECQALSCPHGMAKVPQADSC 1142
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RESULT 14
US-11-149-003-2
; Sequence 2, Application US/11149003
; Publication No. US20060014277A1
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: Novel Human Kiellin-like Proteins and Polynucleotides Encoding the
; FILE REFERENCE: LEX-0360-USA
; CURRENT APPLICATION NUMBER: US/11/149,003
; CURRENT FILING DATE: 2005-06-09
; PRIOR APPLICATION NUMBER: US/10/189,971
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 60/302,949
; PRIOR FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: US 60/315,634
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 1570
; TYPE: PRT
; ORGANISM: homo sapiens
; ORGANISM: Same
US-11-149-003-12
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; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1628
; TYPE: PRT
; ORGANISM: homo sapiens
US-11-149-003-2

Query Match          5.6%; Score 129; DB 11; Length 1628;
Best Local Similarity 20.6%; Pred. No. 0.003;
Matches 92; Conservative 40; Mismatches 185; Indels 130; Gaps 25;

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Db 794 PDPREPCLVCTCLGFGFTTCRRPCCGSHPLIPSGHCCPTCCGCRVHGVTASGETLP 853
Qy 75 LPSEEPSVPADCLAAQNLNSSLIGCMCHRMKNQVACLDIYVTVHRAISLGNVELDVS 134
Db 854 DPLDPTCSLCTCQEGSMRCQKKPCAPALCPHPSPGCFCP-----VCHSCLSQGREHQDGE 909
Qy 135 PYEDTVTSKPW-KMNLKSLKMLKPDSDLCLKF---AMLCTL-----NDKCDRLR--KAYG 183
Db 910 EPEGPAGSCWCRCQAQVS-----CVRLQCPPLPKLQVTERGCCPCRCGCLAHG 961
Qy 184 E-----ACSGPHCQRHVCLRLQTLTFFEKAAEPHAQGLLLCP--CAPNDRGCG 228
Db 962 EEHPGSRWVPPDSACSSCVCHGVVTCARIQCISSCAQPR-QG-----PHDCCPQCSDC- 1015
Qy 229 ERRRTTIAPNCLPVPAPNCLLELRLLCFSDP-----LCRSRLVDFQTHCHPMDIL-- 278
Db 1016 EHEGRKYEPGESFPQGDAPC-----EVCICEFPQEPGPPSLRCHRRQCPSLVGCPCPSQLLPP 1071
Qy 279 -----GTCATEOSRCLRAYLGLIGTAMTNFVSNVNTSVALSCTCRGSGNL-----Q 325
Db 1072 GPQHCCPTCAEALNSCSE--GILGSELAP-----PDCYTCQQQDLTWLCIHQACPE 1121
Qy 326 EECMLEGFFSHNP-----CLTEAIAAKMRFHSQLSQSDWPHPTFAVMA----- 369
Db 1122 LSCPLSE---RHTPPGSCCPVCRVCVEABGRV-----ADGESWRDPSNACIACHTCHRG 1173
Qy 370 -----HQNENPVR-PQPM--VPSLFSC 389
Db 1174 HVECHLEECQALSCPHGWAKVPQADSC 1200

RESULT 15
US-11-169-041-131
; Sequence 131, Application US/11169041
; Publication No. US20060019284A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: IDENTIFICATION OF POLYNUCLEOTIDES FOR PREDICTING ACTIVITY OF
; TITLE OF INVENTION: COMPOUNDS THAT INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE
; TITLE OF INVENTION: KINASES AND/OR PROTEIN TYROSINE KINASE PATHWAYS IN LUNG CANCER
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 10001 NP
; CURRENT APPLICATION NUMBER: US/11/169,041
; CURRENT FILING DATE: 2005-06-28
; PRIOR APPLICATION NUMBER: 60/584,405
; PRIOR FILING DATE: 2004-06-30
; NUMBER OF SEQ ID NOS: 527
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 131
; LENGTH: 2871
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-169-041-131

Query Match          5.6%; Score 123.5; DB 11; Length 2871;
Best Local Similarity 19.3%; Pred. No. 0.019;
Matches 84; Conservative 46; Mismatches 131; Indels 175; Gaps 25;

Qy 48 RRCQADPTCSAAVHHLSDCTSSISTPLPSEEPSVPADCLAAQNLNSSLIG---CMC- 103
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Db 2242 RRNCKDEDECEGKH-----DCTEKQMECKN--LIGTYMCIG 2277
Qy 104 --HRRMKNQVACLD-----IYWTVHRAISLGNVELDVSFYEDTVTSKPWMKNLSKL 152
Db 2278 PGYQRPDGGCVDENECQTKPGICENGRCLNTRGSTTCBEN---DGFTA----- 2324
Qy 153 NMLKPDSDLCLK---FAMLCITLNDKC---DRLRKAYGEACS---GPHCQRHVCL 197
Db 2325 ---SPNQDECLDNREGVCFTFVLQNMCOIGSSNRNPFVTKSECCCGDGRGWGPHCE--ICP 2379
Qy 198 ROLLTFFEKAAEPHAQGLL-----LC---PCAPNDRGCGERRRNTIAPNCA 240
Db 2380 FQGTVAFKKLC-PHGRGFTMGADIDCKVIHVDVRNGECV--NDRG---SYHCICKTY 2433
Qy 241 LPVP-APNCLLELRLLCFSDP-----LCRSRLVDFQTHCHPMDI-----LGTCAE 284
Db 2434 TPDITGTSVDLNE-CNQAPKPCNFKCKWTEGSGYQCSCKPKGYLQEDGRSCKDLDECATK 2492
Qy 285 QSRCLRAYLGLIG---TAMTPNFVSN-----VNTSVALSCTC 318
Db 2493 QHNCQFLCVNTIGGFTCKCPGPGTQHTTSCIDNNECTSDINLCGSKGICQNTPGSFTCEC 2552
Qy 319 R-----GSGNLQEBCEML-----EGFFSH-----NPCL 341
Db 2553 QRGFSLDQTGSSCEDVDECEGNHRCQHGQCNIIIGGYRCSQPGYLOHYQWNCQVDENECL 2612
Qy 342 TEAIAAKMRFHSQLSFS 357
Db 2613 SAHICGGASCHNTLGS 2628
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Job time : 21.5734 secs

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GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 12, 2006, 02:10:01 ; Search time 33.3739 Seconds
(without alignments)
983.470 Million cell updates/sec

Title: US-10-668-936-17
Perfect score: 2131
Sequence: 1 MGLSWSPRPPLMLLVLS.....PRLPILSFILPLILQLTW 397

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*
1: /cgn2_6/ptodata/1/iaa/5_COMB.pdp.*
2: /cgn2_6/ptodata/1/iaa/6_COMB.pdp.*
3: /cgn2_6/ptodata/1/iaa/H_COMB.pdp.*
4: /cgn2_6/ptodata/1/iaa/PCFUS_COMB.pdp.*
5: /cgn2_6/ptodata/1/iaa/RE_COMB.pdp.*
6: /cgn2_6/ptodata/1/iaa/backfiles.pdp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2131	100.0	397	2	US-09-220-528-64
2	2131	100.0	397	2	US-09-187-906-17
3	2131	100.0	397	2	US-09-489-407-17
4	1774	83.2	346	2	US-09-187-906-15
5	1774	83.2	346	2	US-09-489-407-15
6	1646.5	77.3	400	2	US-09-220-528-63
7	1646.5	77.3	400	2	US-09-187-906-21
8	1646.5	77.3	400	2	US-09-949-016-9079
9	1646.5	77.3	400	2	US-09-489-407-21
10	1386	65.0	315	2	US-09-187-906-19
11	1386	65.0	315	2	US-09-489-407-19
12	577.5	27.1	445	2	US-08-861-990-11
13	577.5	27.1	464	2	US-08-957-063-6
14	577.5	27.1	464	2	US-09-487-685-6
15	577.5	27.1	464	2	US-08-802-805D-6
16	577.5	27.1	464	2	US-08-861-990-2
17	577.5	27.1	464	2	US-09-388-316C-6
18	577.5	27.1	664	2	US-08-957-063-18
19	577.5	27.1	664	2	US-09-487-685-18
20	577.5	27.1	664	2	US-08-802-805D-18
21	577.5	27.1	664	2	US-09-388-316C-18
22	574.5	27.0	464	2	US-08-957-063-3
23	574.5	27.0	464	2	US-09-487-685-3
24	574.5	27.0	464	2	US-08-802-805D-3
25	574.5	27.0	464	2	US-09-187-906-13
26	574.5	27.0	464	2	US-08-861-990-9
27	574.5	27.0	464	2	US-09-388-316C-3

28	574.5	27.0	464	2	US-09-489-407-13	Sequence 13, Appl
29	574.5	27.0	664	2	US-08-957-063-16	Sequence 16, Appl
30	574.5	27.0	664	2	US-09-487-685-16	Sequence 16, Appl
31	574.5	27.0	664	2	US-08-802-805D-16	Sequence 16, Appl
32	574.5	27.0	664	2	US-09-388-316C-16	Sequence 16, Appl
33	515	24.2	460	2	US-08-802-805D-22	Sequence 22, Appl
34	515	24.2	460	2	US-09-187-906-11	Sequence 11, Appl
35	515	24.2	460	2	US-09-489-407-11	Sequence 11, Appl
36	513.5	24.1	463	2	US-08-837-199A-10	Sequence 10, Appl
37	513.5	24.1	463	2	US-08-837-199A-12	Sequence 12, Appl
38	513.5	24.1	465	2	US-08-837-199A-2	Sequence 2, Appli
39	513.5	24.1	465	2	US-08-861-990-8	Sequence 8, Appli
40	513.5	24.1	465	2	US-09-388-316C-22	Sequence 22, Appl
41	512.5	24.0	465	2	US-08-837-199A-6	Sequence 6, Appli
42	505.5	23.7	468	2	US-08-802-805D-21	Sequence 21, Appl
43	505.5	23.7	468	2	US-08-837-199A-4	Sequence 4, Appli
44	505.5	23.7	468	2	US-08-860-370-2	Sequence 2, Appli
45	505.5	23.7	468	2	US-09-187-906-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-09-220-528-64
; Sequence 64, Application US/09220528A
; Patent No. 6284540
; GENERAL INFORMATION:
; APPLICANT: Milbrandt, Jeffrey D.
; APPLICANT: Baloh, Robert H.
; TITLE OF INVENTION: Artemin, A No. 6284540el Neurotrophic Factor
; FILE REFERENCE: 6029-7998
; CURRENT APPLICATION NUMBER: US/09/220,528A
; CURRENT FILING DATE: 1998-12-24
; EARLIER APPLICATION NUMBER: 09/218,698
; EARLIER FILING DATE: 1998-12-22
; EARLIER APPLICATION NUMBER: 60/108,148
; EARLIER FILING DATE: 1998-11-12
; EARLIER APPLICATION NUMBER: 09/163,283
; EARLIER FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 120
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 64
; LENGTH: 397
; TYPE: PRT
; ORGANISM: Murine
US-09-220-528-64

Query Match	100.0%	Score	2131	DB	2	Length	397
Best Local Similarity	100.0%	Pred. No.	2.2e-211				
Matches	397	Conservative	0	Mismatches	0	Indels	0
Gaps	0						
Qy	1	MGLSWSPRPPLMLLVLSLWPLGAGNSLATENRFVNSCTQARKKEANPACKAAVQH	60				
Db	1	MGLSWSPRPPLMLLVLSLWPLGAGNSLATENRFVNSCTQARKKEANPACKAAVQH	60				
Qy	61	LGSCCTSLSRPLPLEESAMSDCLEAAEQRLNSLIDCRCHRRMKHQATCLDIYWTVHPA	120				
Db	61	LGSCCTSLSRPLPLEESAMSDCLEAAEQRLNSLIDCRCHRRMKHQATCLDIYWTVHPA	120				
Qy	121	RSIGDYELDVSPYEDVTTSKPKWKNLSKLNMLKPDSDLCKFAMLCYTHDKDRLRKAYG	180				
Db	121	RSIGDYELDVSPYEDVTTSKPKWKNLSKLNMLKPDSDLCKFAMLCYTHDKDRLRKAYG	180				
Qy	181	EACSGIRCORHCLQAOLRSFPEKAASHAOGALLCPAPEDAGGERRNTIAPSCALPS	240				
Db	181	EACSGIRCORHCLQAOLRSFPEKAASHAOGALLCPAPEDAGGERRNTIAPSCALPS	240				
Qy	241	VTNCLDLRSFCRADPLCRSLMDFTQCHPMIDILGTCAEQSRCLRAYLGLIGTAMTPN	300				
Db	241	VTNCLDLRSFCRADPLCRSLMDFTQCHPMIDILGTCAEQSRCLRAYLGLIGTAMTPN	300				
Qy	301	FISKVNTTVALSCTCRSGNLDCEQLRSFSFONPCLVEAIAAKMRFHQLFSDWADS	360				

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Db 301 FISKVNTTVALSCTCGSNLQDECEQLERSFSQNPCLVEATAAKRFRHQLFSQDWADS 360
QY 361 TFSVVOQNSNPALRQLPRLPILSILPLILLQTLW 397
Db 361 TFSVVOQNSNPALRQLPRLPILSILPLILLQTLW 397

RESULT 2
US-09-187-906-17
; Sequence 17, Application US/09187906
; Patent No. 6677135
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC.
; TITLE OF INVENTION: Ret Ligand (RetL) for Stimulating Neural
; TITLE OF INVENTION: and Renal Growth
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Biogen, Inc.
; STREET: 14 Cambridge Center
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02142
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/187,906
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/07726
; FILING DATE: 07-MAY-97
; APPLICATION NUMBER: US 60/017,427
; FILING DATE: 08-MAY-96
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/019,300
; FILING DATE: 07-JUN-96
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/021,859
; FILING DATE: 16-JUL-96
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/043,533
; FILING DATE: 10-APR-97
; ATTORNEY/AGENT INFORMATION:
; NAME: Kaplan, Warren A.
; REGISTRATION NUMBER: 34,199
; REFERENCE/DOCKET NUMBER: A008 PCT CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-679-2400
; TELEFAX: 617-679-2838
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 397 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-187-906-17

Query Match 100.0%; Score 2131; DB 2; Length 397;
Best Local Similarity 100.0%; Pred. No. 2.2e-211;
Matches 397; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MGLSWSRPPLMLLLVLSLPLGAGNSLATENRFVNSCTQARKKCEANPACKAAYQH 60
QY 61 LGSCTSSLSRPLPLEESAMSDADLEAAEQLRNSLIDCRCHRRMKHQATCLDIYVTVHPA 120
Db 61 LGSCTSSLSRPLPLEESAMSDADLEAAEQLRNSLIDCRCHRRMKHQATCLDIYVTVHPA 120
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QY 181 EACSGIRCORHLCLAQLRSFFKAAESHAQGLLLCFCAPEDAGCGGERRENTIAPSCALPS 240
Db 181 EACSGIRCORHLCLAQLRSFFKAAESHAQGLLLCFCAPEDAGCGGERRENTIAPSCALPS 240
QY 241 VTPNCLDLRSFCRADPLCRSLRMDFTQTHCHPMIILGTCTATEOSRCLRAYLGLIGTAMTNP 300
Db 241 VTPNCLDLRSFCRADPLCRSLRMDFTQTHCHPMIILGTCTATEOSRCLRAYLGLIGTAMTNP 300
QY 301 FISKVNTTVALSCTCGSNLQDECEQLERSFSQNPCLVEATAAKRFRHQLFSQDWADS 360
Db 301 FISKVNTTVALSCTCGSNLQDECEQLERSFSQNPCLVEATAAKRFRHQLFSQDWADS 360
QY 361 TFSVVOQNSNPALRQLPRLPILSILPLILLQTLW 397
Db 361 TFSVVOQNSNPALRQLPRLPILSILPLILLQTLW 397

RESULT 3
US-09-489-407-17
; Sequence 17, Application US/09489407
; Patent No. 6861509
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC.
; TITLE OF INVENTION: Ret Ligand (RetL) for Stimulating Neural
; TITLE OF INVENTION: and Renal Growth
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Biogen, Inc.
; STREET: 14 Cambridge Center
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02142
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/489,407
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/07726
; FILING DATE: 07-MAY-97
; APPLICATION NUMBER: US 60/017,427
; FILING DATE: 08-MAY-96
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/019,300
; FILING DATE: 07-JUN-96
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/021,859
; FILING DATE: 16-JUL-96
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/043,533
; FILING DATE: 10-APR-97
; ATTORNEY/AGENT INFORMATION:
; NAME: Kaplan, Warren A.
; REGISTRATION NUMBER: 34,199
; REFERENCE/DOCKET NUMBER: A008 PCT CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-679-2400
; TELEFAX: 617-679-2838
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 397 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
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; MOLECULE TYPE: protein
US-09-489-407-17

Query Match      100.0%; Score 2131; DB 2; Length 397;
Best Local Similarity 100.0%; Pred. No. 2.2e-211;
Matches 397; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGLSWSRPPLMTLLVLSLWPLGAGNSLATENRFVNSCTQARKKCEANPACKAAAYQH 60
Db 1 MGLSWSRPPLMTLLVLSLWPLGAGNSLATENRFVNSCTQARKKCEANPACKAAAYQH 60
Qy 61 LGSCTSSSLPPLLEESAMSDCLEAAEQLRNSLIIDCRCHRRMKHOATCLDIYTWHPA 120
Db 61 LGSCTSSSLPPLLEESAMSDCLEAAEQLRNSLIIDCRCHRRMKHOATCLDIYTWHPA 120
Qy 121 RSLGDIYELDVSPYEDTTSKPKWNLSKLNMLKPDSDLCKLFAMLCTLHDKCDRLRKAYG 180
Db 121 RSLGDIYELDVSPYEDTTSKPKWNLSKLNMLKPDSDLCKLFAMLCTLHDKCDRLRKAYG 180
Qy 181 EACSGIRCQRHLCLAQLRSPFEKAASHAQGLLPCAPEDAGCGERRRNTIAPSCALPS 240
Db 181 EACSGIRCQRHLCLAQLRSPFEKAASHAQGLLPCAPEDAGCGERRRNTIAPSCALPS 240
Qy 241 VTPNCLDLRSFCRADPLCRSRLMDFOTHCHPMDILGTCAEQSRCLRAYLGLIGTAMTPN 300
Db 241 VTPNCLDLRSFCRADPLCRSRLMDFOTHCHPMDILGTCAEQSRCLRAYLGLIGTAMTPN 300
Qy 301 FISKVNTVALSCTCRSGNQLQDECEQLERSFSQNPCLVEAIAAKMFRHQLFSQDWADS 360
Db 301 FISKVNTVALSCTCRSGNQLQDECEQLERSFSQNPCLVEAIAAKMFRHQLFSQDWADS 360
Qy 361 TFSVVOQNSNPALRLQPLPILSILPLILLQTLW 397
Db 361 TFSVVOQNSNPALRLQPLPILSILPLILLQTLW 397

RESULT 4
US-09-187-906-15
; Sequence 15, Application US/09187906
; Patent No. 6677135
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC.
; TITLE OF INVENTION: Ret Ligand (RetL) for Stimulating Neural
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Biogen, Inc.
; STREET: 14 Cambridge Center
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02142
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/187,906
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/07726
; FILING DATE: 07-MAY-97
; APPLICATION NUMBER: US 60/017,427
; FILING DATE: 08-MAY-96
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/019,300
; FILING DATE: 07-JUN-96
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/021,859
; FILING DATE: 16-JUL-96
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 60/043,533
; FILING DATE: 10-APR-97
; ATTORNEY/AGENT INFORMATION:
; NAME: Kaplan, Warren A.
; REGISTRATION NUMBER: 34,199
; REFERENCE/DOCKET NUMBER: A008 PCT CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-679-2400
; TELEFAX: 617-679-2838
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 346 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-187-906-15

Query Match: 83.2%; Score 1774; DB 2; Length 346;
Best Local Similarity 100.0%; Pred. No. 1.3e-174;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 68 LSRPLPLEESAMSDCLEAAEQLRNSLIIDCRCHRRMKHOATCLDIYTWHPARSLGDYE 127
Db 17 LSRPLPLEESAMSDCLEAAEQLRNSLIIDCRCHRRMKHOATCLDIYTWHPARSLGDYE 76
Qy 128 LDVSPYEDTTSKPKWNLSKLNMLKPDSDLCKLFAMLCTLHDKCDRLRKAYGEACSGIR 187
Db 77 LDVSPYEDTTSKPKWNLSKLNMLKPDSDLCKLFAMLCTLHDKCDRLRKAYGEACSGIR 136
Qy 188 QRHLCLAQLRSPFEKAASHAQGLLPCAPEDAGCGERRRNTIAPSCALPSVTPNCLD 247
Db 137 QRHLCLAQLRSPFEKAASHAQGLLPCAPEDAGCGERRRNTIAPSCALPSVTPNCLD 196
Qy 248 LRSFCRADPLCRSRLMDFOTHCHPMDILGTCAEQSRCLRAYLGLIGTAMTPNFSKVT 307
Db 197 LRSFCRADPLCRSRLMDFOTHCHPMDILGTCAEQSRCLRAYLGLIGTAMTPNFSKVT 256
Qy 308 TVALSCTCRSGNQLQDECEQLERSFSQNPCLVEAIAAKMFRHQLFSQDWADSTFSVVOQ 367
Db 257 TVALSCTCRSGNQLQDECEQLERSFSQNPCLVEAIAAKMFRHQLFSQDWADSTFSVVOQ 316
Qy 368 QNSNPALRLQPLPILSILPLILLQTLW 397
Db 317 QNSNPALRLQPLPILSILPLILLQTLW 346

RESULT 5
US-09-489-407-15
; Sequence 15, Application US/09489407
; Patent No. 6861509
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC.
; TITLE OF INVENTION: Ret Ligand (RetL) for Stimulating Neural
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Biogen, Inc.
; STREET: 14 Cambridge Center
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02142
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/489,407
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/07726
```

; FILING DATE: 07-MAY-97
; APPLICATION NUMBER: US 60/017,427
; FILING DATE: 08-MAY-96
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/019,300
; FILING DATE: 07-JUN-96
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/021,859
; FILING DATE: 16-JUL-96
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/043,533
; FILING DATE: 10-APR-97
; ATTORNEY/AGENT INFORMATION:
; NAME: Kaplan, Warren A.
; REGISTRATION NUMBER: 34,199
; REFERENCE/DOCKET NUMBER: A008 PCT CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-679-2400
; TELEFAX: 617-679-2838
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 346 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-489-407-15

Query Match 83.2%; Score 1774; DB 2; Length 346;
Best Local Similarity 100.0%; Pred. No. 1.3e-174;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 68 LSRPLPLESAMSADCLEAAEQRLNSLIDCRCHRMKQATCLDIYVTHPARSLGDYE 127
DB 17 LSRPLPLESAMSADCLEAAEQRLNSLIDCRCHRMKQATCLDIYVTHPARSLGDYE 76
QY 128 LDVSPYEDVTTSKPKWNLSKLNMLKPDSDLCLEKPAQLTLDKCDRLKAYGEACSGIR 187
DB 77 LDVSPYEDVTTSKPKWNLSKLNMLKPDSDLCLEKPAQLTLDKCDRLKAYGEACSGIR 136
QY 188 CQRHLCLAQLRSFFKAEASHAQLLLCPAPEDAGCGERRNTIAPSCALPSVTNCLD 247
DB 137 CQRHLCLAQLRSFFKAEASHAQLLLCPAPEDAGCGERRNTIAPSCALPSVTNCLD 196
QY 248 LRSFCRADPLCRSLMDFTQCHPMDILGTCAEQSRCLRAYLGLIGTAMTNPISKVNT 307
DB 197 LRSFCRADPLCRSLMDFTQCHPMDILGTCAEQSRCLRAYLGLIGTAMTNPISKVNT 256
QY 308 TVALSTCRSGNQLQDECEQLERSFSONPCLVEAIAAKMFRHQLFSQDWDSTFVSQQ 367
DB 257 TVALSTCRSGNQLQDECEQLERSFSONPCLVEAIAAKMFRHQLFSQDWDSTFVSQQ 316
QY 368 QNSNPALRQPLRPILSILPILLLQTLW 397
DB 317 QNSNPALRQPLRPILSILPILLLQTLW 346

RESULT 6
US-09-220-528-63
; Sequence 63, Application US/09220528A
; Patent No. 6284540
; GENERAL INFORMATION:
; APPLICANT: Milbrandt, Jeffrey D.
; TITLE OF INVENTION: Artemin, A No. 6284540el Neurotrophic Factor
; FILE REFERENCE: 6029-7998
; CURRENT APPLICATION NUMBER: US/09/220,528A
; CURRENT FILING DATE: 1998-12-24
; EARLIER APPLICATION NUMBER: 09/218,698
; EARLIER FILING DATE: 1998-12-22
; EARLIER APPLICATION NUMBER: 60/108,148
; EARLIER FILING DATE: 1998-11-12
; EARLIER APPLICATION NUMBER: 09/163,283
; EARLIER FILING DATE: 1998-09-29

; NUMBER OF SEQ ID NOS: 120
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 63
; LENGTH: 400
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-220-528-63

Query Match 77.3%; Score 1646.5; DB 2; Length 400;
Best Local Similarity 77.8%; Pred. No. 2.4e-161;
Matches 305; Conservative 30; Mismatches 56; Indels 1; Gaps 1;

QY 7 PRPP-LLMILLVLSLWPLGAGNSLATENRFVNSCTQARKKCEANPACKAAYOHLGSGT 65
DB 9 PLPPVVLMLLLLPSPPLAAGDPLPTESRLMNSCLQARRKCCQADPTCSAAYHHLDST 68
QY 66 SSLSRPLPLESAMSADCLEAAEQRLNSLIDCRCHRMKQATCLDIYVTHPARSLGD 125
DB 69 SSISTPLPSEEPSVPADCLEAAQRLNSLIGCMCHRRMKQVACLDIYVTHRRARSLGN 128
QY 126 YELDVSPYEDVTTSKPKWNLSKLNMLKPDSDLCLEKPAQLTLDKCDRLKAYGEACSG 185
DB 129 YELDVSPYEDVTTSKPKWNLSKLNMLKPDSDLCLEKPAQLTLDKCDRLKAYGEACSG 188
QY 186 IRCQRHLCLAQLRSFFKAEASHAQLLLCPAPEDAGCGERRNTIAPSCALPSVTNPN 245
DB 189 PHCQRHVCLRLQLTTFEKAAPHAQGLLLCPAPNDRGCGERRNTIAPNCALPPVAPNC 248
QY 246 LDLRSFCRADPLCRSLMDFTQCHPMDILGTCAEQSRCLRAYLGLIGTAMTNPISKV 305
DB 249 LELRLCFSDPLCRSLMDFTQCHPMDILGTCAEQSRCLRAYLGLIGTAMTNPFSNV 308
QY 306 NTVVALSTCRSGNQLQDECEQLERSFSONPCLVEAIAAKMFRHQLFSQDWDSTFVS 365
DB 309 NTSVALSTCRSGNQLQDECEMLEGFFSHNPCLTEAIAAAMRPHLSQLFSQDWPHTFAVM 368
QY 366 QQNSNPALRQPLRPILSILPILLLQTLW 397
DB 369 AHQENPAVRPQWPVPSLFSCTPLPILLLSLW 400

RESULT 7
US-09-187-906-21
; Sequence 21, Application US/09187906
; Patent No. 6671135
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC.
; TITLE OF INVENTION: Ret Ligand (RetL) for Stimulating Neural
; TITLE OF INVENTION: and Renal Growth
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Biogen, Inc.
; STREET: 14 Cambridge Center
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02142
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/187,906
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA: PCT/US97/07726
; APPLICATION NUMBER: 07-MAY-97
; FILING DATE: 07-MAY-97
; APPLICATION NUMBER: US 60/017,427
; FILING DATE: 08-MAY-96
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/019,300

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; FILING DATE: 07-JUN-96
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/021,859
; FILING DATE: 16-JUL-96
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/043,533
; FILING DATE: 10-APR-97
; ATTORNEY/AGENT INFORMATION:
; NAME: Kaplan, Warren A.
; REGISTRATION NUMBER: 34,199
; REFERENCE/DOCKET NUMBER: A008 PCT CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-679-2400
; TELEFAX: 617-679-2838
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 400 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-187-906-21

Query Match 77.3%; Score 1646.5; DB 2; Length 400;
Best Local Similarity 77.8%; Pred. No. 2.4e-161;
Matches 305; Conservative 30; Mismatches 56; Indels 1; Gaps 1;

QY 7 PRPP-LIMILLVLSLWPLGAGNSLATENRFVNSCTQARKKCEANPACKAAAYOHLGSC 65
Db 9 PLPPVVLMLLLPSPPLAAGDPLFTESRLMNSCLQARRKQADPTCSAAVHLLDSC 68
QY 66 SSLSRPLPLEESAMSDCLEAAEQLRNSSLIDCRCHRRMKHQATCLDIYVTVHPARSLG 125
Db 69 SSISTPLPSEPSVPADCLEAAQQLRNSSLIGCMCHRRMKNQVACLDIYVTVHARS LG 128
QY 126 YELDVSPYEDTVTSKPKMNLKLNMLKPDSDILCLKPFAMLC TLHDKCDRLRKAYGEACSG 185
Db 129 YELDVSPYEDTVTSKPKMNLKLNMLKPDSDILCLKPFAMLC TLHDKCDRLRKAYGEACSG 188
QY 186 IRCQRHLCLAQLRSPFEKAESHAQGLLLCPAPEDAGCGERRRNTIAPSCALPSVTPNC 245
Db 189 PHCQRHVCLRLQLTFFFEKAEPHAQGLLLCPAPEDAGCGERRRNTIAPNCALPPVAPNC 248
QY 246 LDLSRCPADPLCRSLRMDPQTHCHPMDILGTCAEQSRCLRAYLGLIGTAMTPNFISKV 305
Db 249 LEURLCFSDPLCRSLRMDPQTHCHPMDILGTCAEQSRCLRAYLGLIGTAMTPNFVSNV 308
QY 306 NTTVALSCTCRSGNLQDECEQLERSFQNPCLVEAIAAKRFRHQLFSQDWDADSTFV 365
Db 309 NTSVALSCTCRSGNLQDECEMLEGFFSHNPCLTEAIAAKRFRHQLFSQDWDADSTFV 368
QY 366 QQQNSNPALRQLPRLPILSILPLILLQTLW 397
Db 369 AHQENPAVRPQPVWPSLFSCTPLPLILLLSLW 400

RESULT 8
US-09-949-016-9079
; Sequence 9079, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012

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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9079
; LENGTH: 400
; TYPE: PRT
; ORGANISM: Human
; US-09-949-016-9079

Query Match 77.3%; Score 1646.5; DB 2; Length 400;
Best Local Similarity 77.8%; Pred. No. 2.4e-161;
Matches 305; Conservative 30; Mismatches 56; Indels 1; Gaps 1;

QY 7 PRPP-LIMILLVLSLWPLGAGNSLATENRFVNSCTQARKKCEANPACKAAAYOHLGSC 65
Db 9 PLPPVVLMLLLPSPPLAAGDPLFTESRLMNSCLQARRKQADPTCSAAVHLLDSC 68
QY 66 SSLSRPLPLEESAMSDCLEAAEQLRNSSLIDCRCHRRMKHQATCLDIYVTVHPARSLG 125
Db 69 SSISTPLPSEPSVPADCLEAAQQLRNSSLIGCMCHRRMKNQVACLDIYVTVHARS LG 128
QY 126 YELDVSPYEDTVTSKPKMNLKLNMLKPDSDILCLKPFAMLC TLHDKCDRLRKAYGEACSG 185
Db 129 YELDVSPYEDTVTSKPKMNLKLNMLKPDSDILCLKPFAMLC TLHDKCDRLRKAYGEACSG 188
QY 186 IRCQRHLCLAQLRSPFEKAESHAQGLLLCPAPEDAGCGERRRNTIAPSCALPSVTPNC 245
Db 189 PHCQRHVCLRLQLTFFFEKAEPHAQGLLLCPAPEDAGCGERRRNTIAPNCALPPVAPNC 248
QY 246 LDLSRCPADPLCRSLRMDPQTHCHPMDILGTCAEQSRCLRAYLGLIGTAMTPNFISKV 305
Db 249 LEURLCFSDPLCRSLRMDPQTHCHPMDILGTCAEQSRCLRAYLGLIGTAMTPNFVSNV 308
QY 306 NTTVALSCTCRSGNLQDECEQLERSFQNPCLVEAIAAKRFRHQLFSQDWDADSTFV 365
Db 309 NTSVALSCTCRSGNLQDECEMLEGFFSHNPCLTEAIAAKRFRHQLFSQDWDADSTFV 368
QY 366 QQQNSNPALRQLPRLPILSILPLILLQTLW 397
Db 369 AHQENPAVRPQPVWPSLFSCTPLPLILLLSLW 400

RESULT 9
US-09-489-407-21
; Sequence 21, Application US/09489407
; Patent No. 6861509
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC.
; TITLE OF INVENTION: Ret Ligand (RetL) for Stimulating Neural
; TITLE OF INVENTION: and Renal Growth
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Biogen, Inc.
; STREET: 14 Cambridge Center
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02142
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/489,407
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/07726
; FILING DATE: 07-MAY-97
; APPLICATION NUMBER: US 60/017,427
; FILING DATE: 08-MAY-96
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/019,300
; FILING DATE: 07-JUN-96

```

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/021,859
; FILING DATE: 16-JUL-96
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/043,533
; FILING DATE: 10-APR-97
; ATTORNEY/AGENT INFORMATION:
; NAME: Kaplan, Warren A.
; REGISTRATION NUMBER: 34,199
; REFERENCE/DOCKET NUMBER: A008 PCT CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-679-2400
; TELEFAX: 617-679-2838
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 400 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-489-407-21

Query Match 77.3%; Score 1646.5; DB 2; Length 400;
Best Local Similarity 77.8%; Pred. No. 2.4e-161;
Matches 305; Conservative 30; Mismatches 56; Indels 1; Gaps 1;

QY 7 PRPP-LLMILLVLSLWPLGAGNSLATENRFVNSCTQARKKEANPACKAAAYQHLGSC 65
DB 9 PLPPVVMILLLLPPSPPLAAGDPLPTESRLMNSCLQARRKQADPTCSAAHYHLLDSC 68

QY 66 SLSRPLPLEESAMSDCLEAARQLRNSLIDCRCHRRMKHQATCLDIYVTHPARSLGD 125
DB 69 SSISTPLPEEESPVPADCLEAARQLRNSLIDCRCHRRMKHQATCLDIYVTHPARSLGN 128

QY 126 YELDVSPYEDTVTSKPKWNLSKLNMLKPDSDCLKPFAMLTLDKCDRLRKAYGACSG 185
DB 129 YELDVSPYEDTVTSKPKWNLSKLNMLKPDSDCLKPFAMLTLDKCDRLRKAYGACSG 188

QY 186 IRCORHLCLAQLSRFEKAAESHAQGLLLCPAPEDAGCGERRNTIAPSCALPSVTPNC 245
DB 189 PHCQRHVCLRLQLTFEKAEPHAQGLLLCPAPEDAGCGERRNTIAPNCALPPVAPNC 248

QY 246 LDLRSFCRADPLCRSLRMDFOYTHCHPMDILGTCAEQSRCLRAYLGLIGTAMTPNFISKV 305
DB 249 LEHLRLCFSDPLCRSLRVDFQTHCHPMDILGTCAEQSRCLRAYLGLIGTAMTPNFVSV 308

QY 306 NTTVALSCTCRSGNLODECEQLERSFSONPCLVEAIAAKMRPHQLFSQDWDADTFSTV 365
DB 309 NTSVALSCTCRSGNLODECEMLEGFFSHNPCLTEAIAAKMRPHQLFSQDWDADTFSTV 368

QY 366 QOONSNPALRLOPLRPLILSILPLILQLTLW 397
DB 369 AHQONENPAVRPQWPVPSLFSCTPLILLLSLW 400

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RESULT 10
US-09-187-906-19
; Sequence 19, Application US/09187906
; Patent No. 6677135
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC.
; TITLE OF INVENTION: Ret Ligand (RetL) for Stimulating Neural
; TITLE OF INVENTION: and Renal Growth
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Biogen, Inc.
; STREET: 14 Cambridge Center
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02142
; COMPUTER READABLE FORM: floppy disk
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/187,906
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA: PCT/US97/07726
; FILING DATE: 07-MAY-97
; APPLICATION NUMBER: US 60/017,427
; FILING DATE: 08-MAY-96
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/019,300
; FILING DATE: 07-JUN-96
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/021,859
; FILING DATE: 16-JUL-96
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/043,533
; FILING DATE: 10-APR-97
; ATTORNEY/AGENT INFORMATION:
; NAME: Kaplan, Warren A.
; REGISTRATION NUMBER: 34,199
; REFERENCE/DOCKET NUMBER: A008 PCT CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-679-2400
; TELEFAX: 617-679-2838
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 315 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-187-906-19

Query Match 65.0%; Score 1386; DB 2; Length 315;
Best Local Similarity 82.2%; Pred. No. 1.4e-134;
Matches 254; Conservative 17; Mismatches 38; Indels 0; Gaps 0;

QY 89 QLRNSSLIDCRCHRRMKHQATCLDIYVTHPARSLGDYELDVSPYEDTVTSKPKWNLSK 148
DB 7 QLRNSSLIGCMCHRRMKHQVACLDIYVTHPARSLGNLYELDVSPYEDTVTSKPKWNLSK 66

QY 149 LNMKPDSDCLKPFAMLTLDKCDRLRKAYGACSGIRCHLCLAQLSRFEKAAESH 208
DB 67 LNMKPDSDCLKPFAMLTLDKCDRLRKAYGACSGPHCQRHVCLRLQLTFEKAEPH 126

QY 209 AQGLLLCPAPEDAGCGERRNTIAPSCALPSVTPNCLDLRSFCRADPLCRSLRMDFOYTH 268
DB 127 AQGLLLCPAPNDRGCGERRNTIAPNCALPPVAPNCLRLRLCFSDPLCRSLRVDFQTH 186

QY 269 CHPMIDILGTCAEQSRCLRAYLGLIGTAMTPNFISKVNTVALSCTCRSGNLODECEQL 328
DB 187 CHPMIDILGTCAEQSRCLRAYLGLIGTAMTPNFVSNVNTVALSCTCRSGNLODECEML 246

QY 329 ERSFSONPCLVEAIAAKMRPHQLFSQDWDADTFSTVVOQNSNPALRLOPLRPLILSIL 388
DB 247 EGFFSHNPCLTEAIAAKMRPHQLFSQDWDADTFSTVVOQNSNPALRLOPLRPLILSIL 306

QY 389 PLILLQLTLW 397
DB 307 PLILLLSLW 315

RESULT 11
US-09-489-407-19
; Sequence 19, Application US/09489407
; Patent No. 6861509
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC.
; TITLE OF INVENTION: Ret Ligand (RetL) for Stimulating Neural
; TITLE OF INVENTION: and Renal Growth
; NUMBER OF SEQUENCES: 21

```


;;
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Biogen, Inc.
 ; STREET: 14 Cambridge Center
 ; CITY: Cambridge
 ; STATE: MA
 ; COUNTRY: USA
 ; ZIP: 02142
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/489,407
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA: PCT/US97/07726
 ; APPLICATION NUMBER: 07-MAY-97
 ; FILING DATE: 07-MAY-97
 ; APPLICATION NUMBER: US 60/017,427
 ; FILING DATE: 08-MAY-96
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 60/019,300
 ; FILING DATE: 07-JUN-96
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 60/021,859
 ; FILING DATE: 16-JUL-96
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 60/043,533
 ; FILING DATE: 10-APR-97
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Kaplan, Warren A.
 ; REGISTRATION NUMBER: 34,199
 ; REFERENCE/DOCKET NUMBER: A008 PCT CIP
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 617-679-2400
 ; TELEFAX: 617-679-2838
 ; INFORMATION FOR SEQ ID NO: 19:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 315 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-09-489-407-19

Query Match 65.0%; Score 1386; DB 2; Length 315;
 Best Local Similarity 82.2%; Pred. No. 1.4e-134;
 Matches 254; Conservative 17; Mismatches 38; Indels 0; Gaps 0;
 QY 89 QLENSLIDCRCHRRMKHQATCLDIYVTHPARSLGDIYELVSPYEDVTTSKPKWNLK 148
 DB 7 QLENSLIGCMCHRRMKVQACLDIYVTHPARSLGDIYELVSPYEDVTTSKPKWNLK 66
 QY 149 LNMKPDSDLCKFAMLTCLHDKDLRLKAYGACSGIRQORHLCLAQRLSPFEKAESH 208
 DB 67 LNMKPDSDLCKFAMLTCLHDKDLRLKAYGACSGIRQORHLCLAQRLSPFEKAESH 126
 QY 209 AGLLLCPAPEDAGCGERRNTIAPSCALPSTPNCLDLRSFCRADPLCRSLMDPOTH 268
 DB 127 AGLLLCPAPEDAGCGERRNTIAPSCALPSTPNCLDLRSFCRADPLCRSLMDPOTH 186
 QY 269 CHPMIDILGTATQSCRLRAYLGLTAMTPNFISKVNTVALSCCTCRSGNLDCEQL 328
 DB 187 CHPMIDILGTATQSCRLRAYLGLTAMTPNFISKVNTVALSCCTCRSGNLDCEQL 246
 QY 329 ERSFQNPCLVEIAAAMRPHRLQFSQDWDADSTFVQQQNSPALRLQPLPILSFSIL 388
 DB 247 EGFSSHNPCLTEIAAKRHFSLQFSQDWDADSTFVQQQNSPALRLQPLPILSFSIL 306
 QY 389 PLILLOTILW 397
 DB 307 PLILLLSLW 315

RESULT 12
 US-08-861-990-11
 ; Sequence 11, Application US/08861990
 ; Patent No. 6698259
 ; GENERAL INFORMATION:
 ; APPLICANT: Ibanez, Carlos F.
 ; APPLICANT: Arumae, Urmas
 ; APPLICANT: Sariola, Hannu
 ; APPLICANT: Suvarato, Petro
 ; APPLICANT: Tuppu, Miles
 ; APPLICANT: Saarna, Mart
 ; TITLE OF INVENTION: Glial Cell Line-Derived Neurotropic Factor Receptors
 ; FILE REFERENCE: CEPH0418
 ; CURRENT APPLICATION NUMBER: US/08/861,990
 ; CURRENT FILING DATE: 1997-05-22
 ; PRIOR APPLICATION NUMBER: 08/747,842
 ; PRIOR FILING DATE: 1996-11-13
 ; PRIOR APPLICATION NUMBER: 60/006,619
 ; PRIOR FILING DATE: 1995-11-13
 ; PRIOR APPLICATION NUMBER: 60/015,767
 ; PRIOR FILING DATE: 1996-04-16
 ; PRIOR APPLICATION NUMBER: 60/021,965
 ; PRIOR FILING DATE: 1996-08-27
 ; PRIOR APPLICATION NUMBER: 60/020,638
 ; PRIOR FILING DATE: 1996-06-27
 ; PRIOR APPLICATION NUMBER: 60/020,639
 ; PRIOR FILING DATE: 1996-06-27
 ; NUMBER OF SEQ ID NOS: 11
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 11
 ; LENGTH: 445
 ; TYPE: PRT
 ; ORGANISM: Rattus sp.
 ; US-08-861-990-11

Query Match 27.1%; Score 577.5; DB 2; Length 445;
 Best Local Similarity 38.8%; Pred. No. 7.2e-51;
 Matches 127; Conservative 40; Mismatches 125; Indels 35; Gaps 9;
 QY 41 CTQARKKCEANPACKAAYQHLGSCSTSSLRPLLESAMSDCLEAEQRLNSLIDCR 100
 DB 40 CVRANELCAABSNCSSRYRTLQCLAGDRDNTWL-----ANKCOALEVLOESPLYDCRC 95
 QY 101 HRRMKHQATCLDIYVTHPARSLGDIYELVSPYEDVTTSKPKWNLKLNML----- 152
 DB 96 KRGKMKELQCLQIYNSIHGLTEGEFEYASPYE-PVTSR-----LSDIFRLASIFSGTG 149
 QY 153 -----KPSDSLCKLFAMLTCLHDKDLRLKAYGEACS-----GIRQORHLCLAQRLSPFE 202
 DB 150 TDPAVSTKSNHCLDAKACNLNDNCKLRSSYISICNREISPTERCNRRKCHKALRQFFD 209
 QY 203 KAASHAQLGCLPCAPEDAGCGERRNTIAPSCAL-PSVTPNCLDLRSFCRADPLCRSR 261
 DB 210 RVSEYTYRMLFCSC--QDQACAEERRRQTLPSCSYEDKEKPNCLDLRLSLCRTDHLCSR 267
 QY 262 LMDFOQHCHP--MDILGTATQSCRLRAYLGLTAMTPNFISKVNTVALS--CTCRG 317
 DB 268 LADFHANCASRYTITSCPADNYOACLGSYAGMIGDMTPNYVDNPTGIVVSPWNCRG 327
 QY 318 SGNLQDECEQLRSFSQNFCLVEAIAA 344
 DB 328 SGNMEECEKFLRDFTFENCLRNAIOA 354

RESULT 13
 US-08-957-063-6
 ; Sequence 6, Application US/08957063
 ; Patent No. 6025157
 ; GENERAL INFORMATION:
 ; APPLICANT: Robert D. Klein, Arnon Rosenthal, Mary A. Hynes
 ; TITLE OF INVENTION: Neurturin Receptor
 ; NUMBER OF SEQUENCES: 19


```

;
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/802,805D
; FILING DATE: 18-Feb-1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Torchia, PhD., Timothy E.
; REGISTRATION NUMBER: 36,700
; REFERENCE/DOCKET NUMBER: P1086
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-8674
; TELEFAX: 650/952-9881
;
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 464 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
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; US-08-802-805D-6
;
; Query Match 27.1%; Score 577.5; DB 2; Length 464;
; Best Local Similarity 38.8%; Pred. No. 7.6e-51;
; Matches 127; Conservative 40; Mismatches 125; Indels 35; Gaps 9;
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; QY 41 CTOARKKCEANPACKAAYQHLSGTSLSRPPLLESAMSADCLEAAEQLENSSLIDCRC 100
; DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
; 40 CVRANELCAEBSNCSSRYRTLROCLAGRDRTNWL-----ANKECQAALVLEQESPLYDCRC 95
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; QY 101 HRRMKHQATCLDIYTWVHPARSLGDYELDVSPYEDYVTSKPMKNLSKLNML----- 152
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; 96 KRGKKELQCLQIYNSIHGLTEGEHFEASPYE-PVTSR-----LSDIFRLASIFSGTG 149
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; QY 153 -----KPDSDLCLKFAMLTLDHDKDRLRKAYGEACS-----GIRCORHLCLAQLSFFE 202
; DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
; 150 TDPAVSTKGNHCLDAAKACMLNDNCKLRSSYSICNREISPTERCNRRKCHKALRQFPD 209
;
; QY 203 KAAESHAQGLLLCPAPEDAGCGERRRNTIAPSCAL-PSVTFNCLDIRSECRADPLCRSR 261
; DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
; 210 RVPEYTYRMLFCSC--QOQACAEERRRQTILPSCSYEDKEKPNCLDLRLSLCRTDHLCSR 267
;
; QY 262 LMDPQTHCHP--MDILGTCAEQSRCLRAYLGLIGTAMTFNFKVNTTVALS--CTCRG 317
; DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
; 268 LADFHANCRASTYITISCPADNYOACLSYAGNIGFDMTFNYVDSNPTGIVVSPWCNCRG 327
;
; QY 318 SGNLQDECEQLERSFSQNPCLVEAIAA 344
; DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
; 328 SGNMEECEKFLRDFTEPCLRNAIOA 354
;
;
; Search completed: May 12, 2006, 02:11:41
; Job time : 34.3739 secs
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GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: May 12, 2006, 01:59:25 ; Search time 140.527 Seconds
(without alignments)
1250.660 Million cell updates/sec

Title: US-10-668-936-21

Perfect score: 2190

Sequence: 1 MVRPLNRPPLPPVVMMLLL.....PWVSLFSCPTLPILLLSLW 400

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_21:*
1: Geneseq1980s:*
2: Geneseq1990s:*
3: Geneseq2000s:*
4: Geneseq2001s:*
5: Geneseq2002s:*
6: Geneseq2003as:*
7: Geneseq2003bs:*
8: Geneseq2004s:*
9: Geneseq2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	2190	100.0	400	2 AAW65116	AAW65116 Human GDN
2	2190	100.0	400	2 AAW37463	AAW37463 Human Ret
3	2190	100.0	400	2 AAW84186	AAW84186 Glial cel
4	2190	100.0	400	3 AAY83226	AAY83226 PRO538 Po
5	2190	100.0	400	3 AAY84590	AAY84590 Amino aci
6	2190	100.0	400	3 AAY15177	AAY15177 Human GFR
7	2190	100.0	400	3 AAB19582	AAB19582 Human PRO
8	2190	100.0	400	3 AAB24411	AAB24411 Human PRO
9	2190	100.0	400	3 AAB00171	AAB00171 PRO538 po
10	2190	100.0	400	3 AAB24050	AAB24050 Human PRO
11	2190	100.0	400	8 ADJ58713	ADJ58713 Human ret
12	2190	100.0	400	8 ADT94302	ADT94302 Human PRO
13	2190	100.0	400	9 ADY53849	ADY53849 Human ret
14	2190	100.0	400	9 ADZ00213	ADZ00213 Human Ret
15	2190	100.0	628	3 AAY15179	AAY15179 GFRalpha3
16	2186	99.8	400	2 AAW84180	AAW84180 A GDNFR-a
17	2184	99.7	400	2 AAW65117	AAW65117 Human GDN
18	2043	93.3	378	2 AAW84185	AAW84185 Glial cel
19	1996.5	91.2	369	3 AAY15178	AAY15178 Human GFR
20	1996.5	91.2	369	3 AAB19583	AAB19583 Human PRO
21	1996.5	91.2	369	3 AAB24051	AAB24051 Human PRO
22	1708	78.0	315	2 AAW37462	AAW37462 Human Ret
23	1708	78.0	315	8 ADJ58711	ADJ58711 Human ret
24	1708	78.0	315	9 ADY53847	ADY53847 Partial h

25	1708	78.0	315	9	ADZ00211	Adz00211 Human Ret
26	1646.5	75.2	397	2	AAW37461	AAW37461 Mouse Ret
27	1646.5	75.2	397	3	AAAY84591	Aay84591 Amino aci
28	1646.5	75.2	397	3	AAAY15174	Aay15174 Murine GF
29	1646.5	75.2	397	8	ADJ58709	Adj58709 Murine re
30	1646.5	75.2	397	9	ADY53845	Ady53845 Mouse ret
31	1646.5	75.2	397	9	ADZ00209	Adz00209 Mouse Ret
32	1642.5	75.0	397	2	AAW84182	AAW84182 A GDNFR-a
33	1567	71.6	888	3	AAAY15182	Aay15182 GD-GFRalp
34	1455	66.4	346	2	AAW37465	AAW37465 Mouse Ret
35	1455	66.4	346	8	ADJ58707	Adj58707 Murine re
36	1455	66.4	346	9	ADY53843	Ady53843 Partial m
37	1455	66.4	346	9	ADZ00207	Adz00207 Mouse Ret
38	1064	48.6	366	9	AEA39229	Aea39229 GRAL-rela
39	944	43.1	172	2	AAW65118	AAW65118 Human GDN
40	632.5	28.9	498	2	AAW84183	AAW84183 Consensus
41	589.5	26.9	489	2	AAW84298	AAW84298 Consensus
42	547.5	25.0	460	2	AAW84181	AAW84181 A GDNFR-a
43	544.5	24.9	411	2	AAW81625	AAW81625 Mouse mat
44	544.5	24.9	463	2	AAW81624	AAW81624 Mouse TGF
45	543.5	24.8	951	3	AAAY15180	Aay15180 GD-GFRalp

ALIGNMENTS

RESULT 1
AAW65116
ID AAW65116 standard; protein; 400 AA.
XX
AC AAW65116;
XX
DT 28-SEP-1998 (first entry)
XX
DE Human GDNF alpha-3 receptor protein #1.
XX
KW Glial cell line-derived neurotrophic factor alpha-3 receptor; GDNF;
KW treatment; neurodegenerative disease; Parkinson's Disease; ALS; SMA;
KW amyotrophic lateral sclerosis; spinal muscular atrophy; nerve; trauma;
KW Huntington's Disease; Alzheimer's Disease; diabetic neuropathy; muscle;
KW muscular dystrophy; diagnostic.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Protein 1..400
FT /label= GDNF alpha-3
FT /note= "Partial sequence"
XX
EP846764-A2.
PD 10-JUN-1998.
XX
PF 20-NOV-1997; 97EP-00309375.
XX
PR 27-NOV-1996; 96GB-00024677.
PR 09-MAY-1997; 97GB-00009463.
XX
PA (SMIK) SMITHKLINE BEECHAM PLC.
XX
PI Lawrence GMP;
PI WPI; 1998-299980/27.
DR N-PSDB; AAV35364.
XX
PT New factor alpha 3 receptor polypeptide and e.g. DNA and agonists - used
PT to treat neuro degenerative diseases, muscular diseases and nerve and
PT muscle trauma and in diagnostic assays.
XX
PS Claim 4; Fig 2; 22pp; English.
XX
CC This sequence represents a novel glial cell line-derived neurotrophic
CC factor alpha-3 receptor (GDNF alpha-3). This protein can be used to treat

e.g. neurodegenerative diseases (such as Parkinson's Disease, amyotrophic lateral sclerosis (ALS), spinal muscular atrophy (SMA), Huntington's Disease, Alzheimer's Disease, diabetic neuropathy), muscular diseases (including the muscular dystrophies) and nerve and muscle trauma and in diagnostic assays for such conditions

XX
SQ Sequence 400 AA;

Query Match 100.0%; Score 2190; DB 2; Length 400;
Best Local Similarity 100.0%; Pred. No. 1.5e-193;
Matches 400; Conservative 0; Mismatches 0; Indels 0

Qy	1	MYRPLNRPRLPPVWLMILLILPPSPPLPLAAGDPLPTESRLMNSCLQARRKCOADPTCSAA	60
Db	1	MYRPLNRPRLPPVWLMILLILPPSPPLPLAAGDPLPTESRLMNSCLQARRKCOADPTCSAA	60
Qy	61	YHHLDSCTSSISTPLPSPSEPSVPADCLAEAAQOLRNSSLIGCMCHRRMNQOVACLDIYWTV	120
Db	61	YHHLDSCTSSISTPLPSPSEPSVPADCLAEAAQOLRNSSLIGCMCHRRMNQOVACLDIYWTV	120
Qy	121	HRARISLGNLYELDVSPYEDVTVTSKPMKNLSKLNMLKPDSDLCKLFAMLCTLNDKCDRLRK	180
Db	121	HRARISLGNLYELDVSPYEDVTVTSKPMKNLSKLNMLKPDSDLCKLFAMLCTLNDKCDRLRK	180
Qy	181	AYGEACSGPHCORHVCILRQLITFFEKAAPHAQGLLPCAPANDRGCGERRRNTIAPNCA	240
Db	181	AYGEACSGPHCORHVCILRQLITFFEKAAPHAQGLLPCAPANDRGCGERRRNTIAPNCA	240
Qy	241	LPPVAPNCLLEIRLFCSDPLCRSLVDFOTHCHPMDILGTCAEQSQRCLRAYLGLIGTAM	300
Db	241	LPPVAPNCLLEIRLFCSDPLCRSLVDFOTHCHPMDILGTCAEQSQRCLRAYLGLIGTAM	300
Qy	301	TNPFVSNVNTSVALSCTCRGSGNLQOECEMLEGFFSHNPCLTEAIAAKMRFHSQLPSQDW	360
Db	301	TNPFVSNVNTSVALSCTCRGSGNLQOECEMLEGFFSHNPCLTEAIAAKMRFHSQLPSQDW	360
Qy	361	PHPTFAVMAHONENPAVRPQWPVPSLFCSTLPLILLISLW	400
Db	361	PHPTFAVMAHONENPAVRPQWPVPSLFCSTLPLILLISLW	400

RESULT 2

RESOL 2
AAW37463
ID AAW37463 standard: protein: 400 AA.

AA AAW37463;

21-MAY-1998 (first entry)

Human Ret Ligand RetL3.

Ret ligand; RetL; RetL3; receptor; signal transduction; human;
cell growth; renal cell; nerve cell; renal failure; nephritis;
kidney transplant; toxic injury; hypoxic injury; neurodegeneration;
motor neuron disease; multiple sclerosis; infection; meningitis;
myelopathy; Creutzfeldt-Jakob disease; cranial nerve injury;
spinal cord injury; Down's syndrome; cerebral palsy; Lyme disease;
muscular atrophy; myasthenia gravis; tumour; therapy.

XX Homo sapiens.

XX
PN
WO9744356-A2.XX
PD
27-NOV-1997.

XX
PF 07-MAY-1997: 97WO-US007726.

08-MAY-1996: 96US-0017427P.

PR 07-JUN-1996; 96US-0015300E:
PR 16-JUL-1996; 96US-0021859P:

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XX	Sanicola-Nadel M, Hession C, Cate RL;
PI	
XX	WPI; 1998-018431/02.
DR	N-PSDB; AAV00251.
DR	
XX	
XX	New nucleic acid encoding ret receptor ligands and related proteins -
PT	vectors, transformed cells and antibodies, used for promoting cell growth
PT	and improving survival of injured cells, especially renal or nerve cells.
XX	
XX	Claim 2; Page 85-86; 113pp; English.
PS	

This amino acid sequence comprises human Ret ligand (RetL) RetL3, deduced from cDNA clones (see AAV00251) isolated from a adult heart and spinal cord libraries. Rat and mouse RetL3, human RetL2 and mouse RetL3 sequences (see AAV37457-62) are also claimed. Human RetL3 is 34.3% identical to human RetL1, 34.9% identical to human RetL2 and 76.8% identical to murine RetL3. Ret ligand is a key component of the Ret signalling pathway that specifically interacts with Ret receptor protein, triggering Ret dimerisation and/or autophosphorylation of the Ret tyrosine kinase domain. Vectors containing RetL3 DNA and prokaryotic or eukaryotic host cells transformed or transfected with these vectors are claimed, as well as a method for production of RetL3, its soluble variants and fusion proteins with a toxin, imageable compound or radionuclide. RetL3, optionally when expressed from vectors *in vivo*, is used to promote growth of new tissue and survival of damaged tissue, particularly kidney or neural tissue. Typical applications are in renal failure, nephritis, kidney transplants, toxic or hypoxic injury, neurodegeneration, motor neurone disease, multiple sclerosis, bacterial, viral or prion infections (e.g. meningitis, myelopathy associated with HIV or Creutzfeldt-Jakob disease), cranial nerve or spinal cord injury, developmental disorders such as Down's syndrome and cerebral palsy, or conditions involving the peripheral nervous system (lyme disease, muscular dystrophy and myasthenia gravis). Fusion proteins are used to deliver toxins etc. to Ret-expressing cells, especially tumours

Sequence 400 AA:

Query Match 100.0%; Score 2190; DB 2; Length 400;
Best Local Similarity 100.0%; Pred. No. 1.5e-193;
Matches 400; Conservative 0; Mismatches 0; Indels 0

Qy	1	MVRPLNRPPLPPVVLMLLLLLPSPPLAAGDPLPTESRLMNSCLQARRKCOADPTCSAA	60
Db	1	MVRPLNRPPLPPVVLMLLLLLPSPPLAAGDPLPTESRLMNSCLQARRKCOADPTCSAA	60
Qy	61	YHHLDSCTSSISTPLPEEPSVPADCLEAAQAQRNSSLIGCMCHRRMNQVACLDIYWTV	120
Db	61	YHHLDSCTSSISTPLPEEPSVPADCLEAAQAQRNSSLIGCMCHRRMNQVACLDIYWTV	120
Qy	121	HRARSLGNVELDYSPYEDVTTSKPWKNNLSKLNMCLKFAMLTCLNDKCDSLRLK	180
Db	121	HRARSLGNVELDYSPYEDVTTSKPWKNNLSKLNMCLKFAMLTCLNDKCDSLRLK	180
Qy	181	AYGEACSGPHCQRHVLCRQLLTFEFAAEPAHQGLLLCPCAPNDRGGERRRNTIAPNCA	240
Db	181	AYGEACSGPHCQRHVLCRQLLTFEFAAEPAHQGLLLCPCAPNDRGGERRRNTIAPNCA	240
Qy	241	LPVPAPNCLELRILCFSDPLCRSRLVDFOFHCHPMIDLGTCAQSCLRAYLGLIGTAM	300
Db	241	LPVPAPNCLELRILCFSDPLCRSRLVDFOFHCHPMIDLGTCAQSCLRAYLGLIGTAM	300
Qy	301	TPNFVSNVNTSVALSCTCRSGNMQECEMLEGFFFSHNPCLTEIAAKMRPHSLFSQDW	360
Db	301	TPNFVSNVNTSVALSCTCRSGNMQECEMLEGFFFSHNPCLTEIAAKMRPHSLFSQDW	360
Qy	361	PHPTFAVMAHONENPAVRPOPWPVPSLFCSTLPLILLLSLV	400
Db	361	PHPTFAVMAHONENPAVRPOPWPVPSLFCSTLPLILLLSLV	400

RESULT 3

AAW84186

ID AAW84186 standard; protein; 400 AA.
 XX AAW84186;
 XX
 DT 25-MAR-1999 (first entry)
 XX
 DE Glial cell line-derived neurotrophic factor receptor gamma 2.
 XX
 KW Glial cell line-derived neurotrophic factor receptor gamma 2;
 KW GDNFR-alpha; glial cell line-derived neurotrophic factor; GDNF;
 KW neurodegenerative disease; amyotrophic lateral sclerosis; GDNFR-gamma2;
 KW Parkinson's disease; schizophrenia; insomnia; tardive dyskinesia;
 KW hyperextension; pituitary adenomas; hyperprolactinemia; thyroid tumour;
 KW renal disorder; kidney failure; gut dysfunction; regeneration;
 KW cardiomyocyte; epithelium; hepatocyte.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..31
 FT /label= signal_peptide
 FT Protein 32..400
 FT /label= mature_protein
 FT Domain 32..382
 FT /note= "extracellular domain"
 FT Domain 383..400
 FT /note= "transmembrane domain"
 XX
 PN W09853069-A2.
 XX
 XX 26-NOV-1998.
 XX
 XX 20-MAY-1998; 98WO-US010328.
 XX
 XX 20-MAY-1997; 97US-0047092P.
 PR 27-JUN-1997; 97US-00884638.
 XX
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX
 XX Ni J, Hau T, Young P, Gentz RL, Ruben SM;
 XX WPI; 1999-070150/06.
 DR N-PSDB; AAV99334.
 XX
 XX New isolated glial cell derived neurotrophic factor receptors - used to
 PT develop products for treating e.g. neurodegenerative disorders,
 PT schizophrenia, hypertension, tumours, renal disorders, kidney failure or
 PT gut dysfunction.
 XX
 PS Claim 53; Fig 7A-D; 156pp; English.
 XX
 CC The present sequence represents a glial cell line-derived neurotrophic
 CC factor receptor gamma 2 (GDNFR-gamma2). GDNFR-gamma2 shares high homology
 CC with GDNFR-alpha, which is capable of complexing with glial cell line-
 CC derived neurotrophic factor (GDNF) and mediating cell response to GDNF.
 CC The GDNFR polypeptides and agonists can be used for treating disorders
 CC associated with decreased activity of the respective polypeptides. They
 CC can be used for treating neurodegenerative diseases such as amyotrophic
 CC lateral sclerosis, Parkinson's disease, schizophrenia, insomnia, tardive
 CC dyskinesia, hypertension, pituitary adenomas, hyperprolactinemia, thyroid
 CC tumour, renal disorders, kidney failure, gut dysfunction, or for
 CC regeneration of cardiomyocytes, epithelium or hepatocytes. Antagonists of
 CC the polypeptides can be used for treating disorders associated with
 CC increased activity of the respective polypeptides. The products can also
 CC be used for detection, diagnosis and drug screening
 XX
 SQ Sequence 400 AA;
 Query Match 100.0%; Score 2190; DB 2; Length 400;
 Best Local Similarity 100.0%; Pred. No. 1.5e-193;
 Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MVRPLNPRPLPPVVLMLLLLPSPPLAAGDPLPTESRLMNSCLQARRKCOADPTCSAA 60

1 MVRPLNPRPLPPVVLMLLLLPSPPLAAGDPLPTESRLMNSCLQARRKCOADPTCSAA 60
 61 YHLDSCSTSTPLPSEEPSVPADCLAAQQLRNSLIGCMCHRRMKNQVACLDIYWTV 120
 61 YHLDSCSTSTPLPSEEPSVPADCLAAQQLRNSLIGCMCHRRMKNQVACLDIYWTV 120
 121 HRARSLGNLYELDVSPYEDTTSKPKWKNLSKJNMLKPDSDILGTCATQSRCLRAYLGLGTAM 180
 121 HRARSLGNLYELDVSPYEDTTSKPKWKNLSKJNMLKPDSDILGTCATQSRCLRAYLGLGTAM 180
 181 AYSGACSGPHCORHVCLRLQLLTFPEKAAEPHAQGLLCPGPNDRGGCGRRRTIAPNCA 240
 181 AYSGACSGPHCORHVCLRLQLLTFPEKAAEPHAQGLLCPGPNDRGGCGRRRTIAPNCA 240
 241 LPVAPNCLRLRLCFSDPLCRSLRVDFQTHCHPMDILGTCATQSRCLRAYLGLGTAM 300
 241 LPVAPNCLRLRLCFSDPLCRSLRVDFQTHCHPMDILGTCATQSRCLRAYLGLGTAM 300
 301 TPNFVSNVNTSVALSCTCRSGNLQEECEMLEGFFSHNPCLTEAIAAMRPHSOLFQSDW 360
 301 TPNFVSNVNTSVALSCTCRSGNLQEECEMLEGFFSHNPCLTEAIAAMRPHSOLFQSDW 360
 361 PHPTFAVMAHQENPAPVRPOPVPVPSLFTPLILLLSLW 400
 361 PHPTFAVMAHQENPAPVRPOPVPVPSLFTPLILLLSLW 400
 RESULT 4
 AAY83226
 ID AAY83226 standard; protein; 400 AA.
 XX
 AC AAY83226;
 XX
 DT 16-AUG-2000 (first entry)
 XX
 DE PRO538 Polypeptide.
 XX
 KW Inhibition; cancer; neoplasia; tumour; breast; ovary; renal; colorectal;
 KW uterus; prostate; lung; bladder; central nervous system; CNS; melanoma;
 KW leukaemia; PRO211; PRO228; PRO538; PRO172; PRO182; human.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..26
 FT /label= Signal_peptide
 FT Modified-site 95..99
 FT /note= "N-glycosylation site"
 FT Modified-site 134..138
 FT /note= "Casein kinase II phosphorylation site"
 FT Modified-site 148..152
 FT /note= "N-glycosylation site"
 FT Modified-site 170..174
 FT /note= "Casein kinase II phosphorylation site"
 FT Modified-site 202..206
 FT /note= "Casein kinase II phosphorylation site"
 FT Modified-site 231..235
 FT /note= "cAMP and cGMP dependent protein kinase phosphorylation site"
 FT Modified-site 279..285
 FT /note= "N-myristoylation site"
 FT Modified-site 294..300
 FT /note= "N-myristoylation site"
 FT Binding-site 305..317
 FT /label= Prokaryotic membrane lipoprotein lipid attachment site
 FT Modified-site 309..313
 FT /note= "N-glycosylation site"
 FT Domain 379..395
 FT /label= Transmembrane_domain
 FT Binding-site 379..390
 FT /label= Prokaryotic membrane lipoprotein lipid attachment


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FT site
XX WO200021996-A2.
XX 20-APR-2000.
XX 05-OCT-1999; 99WO-US023089.
XX 13-OCT-1998; 98US-0104080P.
XX (GETH ) GENENTECH INC.
XX Ashkenazi A, Goddard A, Gurney AL, Klein RD, Napier M, Wood WI,
PI Yuan J;
XX WPI; 2000-317943/27.
XX N-PSDB; AA293702.
XX Composition for inhibiting neoplastic cell growth and treating cancers of
PT ovary, uterus, prostate, lung and bladder, comprises PRO211, PRO228,
PT PRO538, PRO172 or PRO182 polypeptide or their agonist.
XX Claim 10; Fig 6; 122pp; English.
XX Compositions comprising a PRO211, PRO228, PRO538, PRO172 or PRO182
CC polypeptide or their agonist, mixed with a carrier is useful for
CC inhibiting neoplastic growth and treating tumors such as cancers of
CC breast, ovary, renal, colorectal, uterus, prostate, lung, bladder,
CC central nervous system, melanoma and leukaemia
XX
XX Sequence 400 AA;
Query Match 100.0%; Score 2190; DB 3; Length 400;
Best Local Similarity 100.0%; Pred. No. 1.5e-193;
Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MVRPLNRPPLPVVLMILLPLPSPLAAGDPLPTESRLMNSCLQARRKQADPTCSAA 60
DB 1 MVRPLNRPPLPVVLMILLPLPSPLAAGDPLPTESRLMNSCLQARRKQADPTCSAA 60
QY 61 YHLDSTCTSIPTLPSEEPSVPADCLEAAQQLRNSLLIGCMCHRRMKNQVACLDIYTV 120
DB 61 YHLDSTCTSIPTLPSEEPSVPADCLEAAQQLRNSLLIGCMCHRRMKNQVACLDIYTV 120
QY 121 HRARSLGNYELDVSPYEDTTSKPKWKNLSKLNKLPDSDCLKFMCLTINDKCDRLK 180
DB 121 HRARSLGNYELDVSPYEDTTSKPKWKNLSKLNKLPDSDCLKFMCLTINDKCDRLK 180
QY 181 AYGEACGPHCORHVCRLQLLTFFEKAAEPHAQGLLLCPAPNDRGCGERRRNTIAPNCA 240
DB 181 AYGEACGPHCORHVCRLQLLTFFEKAAEPHAQGLLLCPAPNDRGCGERRRNTIAPNCA 240
QY 241 LPPVAPNCLRLCFSDPLCRSRLVDFQTHCHPMDILGTCAEQSRCLRAYLGLGTAM 300
DB 241 LPPVAPNCLRLCFSDPLCRSRLVDFQTHCHPMDILGTCAEQSRCLRAYLGLGTAM 300
QY 301 TPNFVSNVNTSVALSCTCRSGMQLQECMELEGGFFSHNPCLTIAAAMKRFHSLQFSQW 360
DB 301 TPNFVSNVNTSVALSCTCRSGMQLQECMELEGGFFSHNPCLTIAAAMKRFHSLQFSQW 360
QY 361 PHPTFAVMQHONENPAVRPQWPVPSFLSCTPLILLISLW 400
DB 361 PHPTFAVMQHONENPAVRPQWPVPSFLSCTPLILLISLW 400
RESULT 5
AAV84590
ID AAY84590 standard; protein; 400 AA.
XX
XX AAY84590;
XX
XX 25-JUL-2000 (first entry)
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DE Amino acid sequence of a human growth factor receptor-alpha precursor.
XX Human; artemin; growth factor; neurotrophic factor; trophic support;
KW neuron; trigeminal ganglion neuron; nodose ganglion neuron;
KW superior cervical ganglion neuron; midbrain neuron; Alzheimer's disease;
KW peripheral neuropathy; amyotrophic lateral sclerosis; ischemic stroke;
KW Parkinson's disease; Huntington's disease; acute brain injury;
KW acute spinal cord injury; nervous system tumour; blastoma;
KW multiple sclerosis; infection; enteric disease; idiopathic constipation;
KW Parkinson's disease; small cell lung carcinoma.
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FH Peptide 1..31
FT /note= "signal peptide"
FT Protein 32..372
FT /note= "mature protein"
FT Modified-site 95
FT /note= "putative N-linked glycosylation site"
FT Modified-site 148
FT /note= "putative N-linked glycosylation site"
FT Modified-site 309
FT /note= "putative N-linked glycosylation site"
XX WO200018799-A1.
XX 06-APR-2000.
XX 29-SEP-1999; 99WO-US022604.
XX 29-SEP-1998; 98US-00163283.
XX 12-NOV-1998; 98US-0108148P.
XX 22-DEC-1998; 98US-00218698.
XX (UNIW ) UNIV WASHINGTON.
XX Milbrandt JD, Baloh RH;
XX WPI; 2000-293109/25.
XX Isolated artemin growth factor proteins and the nucleic acids that encode
PT them, useful for treating a range of degenerative neuronal disorders such
PT as Parkinson's disease and Huntington's disease.
XX Disclosure; Fig 12; 96pp; English.
XX The present sequence represents a human growth factor receptor-alpha
CC precursor. The specification describes an artemin growth factor protein.
CC Artemin is a neurotrophic factor that belongs to the GDNF (glial cell
CC line-derived neurotrophic factor)/neurturin/persephin family of growth
CC factors and promotes differentiation, maintains mature phenotype and
CC provides trophic support, promoting growth and survival of neurons.
CC Artemin promotes the survival of trigeminal ganglion neurons, nodose
CC ganglion neurons, superior cervical ganglion neurons and tyrosine-
CC hydroxylase-expressing dopaminergic ventral midbrain neurons. Artemin is
CC the only member of the GDNF family that binds to GFR-alpha (growth factor
CC receptor-alpha) and activates the GFR-alpha3/RET (Ret protein- tyrosine
CC kinase) receptor complex and additionally, like GDNF and neurturin,
CC artemin also binds to and activates GFRalpha/RET. Artemin polypeptides
CC and polynucleotides are administered to treat peripheral neuropathy,
CC amyotrophic lateral sclerosis, Alzheimer's disease, Parkinson's disease,
CC Huntington's disease, ischemic stroke, acute brain injury, acute spinal
CC cord injury, a nervous system tumour (e.g. blastoma), multiple
CC sclerosis, infection or enteric disease (e.g. idiopathic constipation or
CC constipation associated with Parkinson's disease, spinal cord injury or
CC use of opiate pain killers). They may also be used to treat a patient
CC suffering from small cell lung carcinoma
XX
XX Sequence 400 AA;
Query Match 100.0%; Score 2190; DB 3; Length 400;
Best Local Similarity 100.0%; Pred. No. 1.5e-193;

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FT Modified-site 95..99 /note= "Aen is N-glycosylated"
 FT Modified-site 148..152 /note= "Aen is N-glycosylated"
 FT Modified-site 231..235 /note= "O-phosphorylated"
 FT Modified-site 279..285 /note= "N-myristoylation"
 FT Modified-site 294..300 /note= "N-myristoylation"
 FT Binding-site 306..317 /note= "prokaryotic membrane lipoprotein lipid attachment site"
 FT Modified-site 309..313 /note= "Aen is N-glycosylated"
 FT Binding-site 379..390 /note= "prokaryotic membrane lipoprotein lipid attachment site"
 XX WO200053760-A2.
 XX 14-SEP-2000.
 XX 10-MAR-2000; 2000WO-US006319.
 XX 12-MAR-1999; 99US-0123957P.
 XX (GETH) GENENTECH INC.
 XX Ferrara N, Goddard A, Gurney AL, Hebert C, Henzel WJ;
 PI Kabakoff RC, Klein RD, Kljavin IJ, Kuo SS, La Fleur M, Wood WI;
 DR WPI; 2000-587437/55.
 DR N-PSDB; AAA88519.
 XX Novel PRO polypeptides useful for preventing or rescuing retinal cells
 PT from injury caused by ocular diseases such as retinitis pigmentosa,
 PT retinopathy, retinal degenerative diseases, degenerative myopia, uveitis.
 XX Claim 2; Fig 14; 140pp; English.
 XX The present sequence is that of human PRO538, as predicted from a cDNA
 CC clone (see AAA8519) isolated from a foetal lung tissue cDNA library
 CC using probes and primers (see AAA8539-41) based on a cDNA clone isolated
 CC from an expressed sequence tag database screening using murine GFR-alpha-
 CC 3. PRO538 has a predicted mol.wt. of 44,511 and a pI of about 8.15. A
 CC splice variant (PRO3664, see AAB19583) of PRO538 was also identified;
 CC PRO3664 has a 31-amino acid deletion (amino acid positions 127-157 of
 CC PRO538). The invention provides a method for producing PRO polypeptides,
 CC including PRO538, using a host cell transformed with a vector comprising
 CC a PRO nucleic acid is claimed. The invention relates to the use of PRO
 CC polypeptides to delay, prevent or rescue retinal cells such as retinal
 CC neurons selected from photoreceptors, retinal ganglion cells, displaced
 CC retinal ganglion cells, amacrine cells, displaced amacrine cells,
 CC horizontal and bipolar neurons, and supportive cells (including Mueller
 CC cells and pigment epithelial cells) from injury and degradation. The
 CC retinal cells are preferably photoreceptors and photoreceptor cell injury
 CC or death is caused by retinal injury, light or environmental trauma or by
 CC an ocular disease selected from retinitis pigmentosa, macular
 CC degeneration, including age-related, retinal detachment, retinal tears,
 CC retinopathy, retinal degenerative diseases, macular holes, degenerative
 CC myopia, acute retinal necrosis syndrome, traumatic chorioretinopathies or
 CC contusion such as Purtscher's retinopathy, edema, ischemic conditions
 CC such as central or branch retinal vision occlusion, collagen vascular
 CC diseases, thrombocytopenic purpura, uveitis, retinal vasculitis and
 CC occlusion associated with Eales disease and systemic lupus erythematosus
 CC (claimed)
 XX Sequence 400 AA;
 SQ Query Match 100.0%; Score 2190; DB 3; Length 400;
 Best Local Similarity 100.0%; Pred. No. 1.5e-193;
 Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVRPLNRPPLPVVLMILLIPPSPLPLAAGDPLPTESLMNSCLQARRKCOADPTCSAA 60
 DB 1 MVRPLNRPPLPVVLMILLIPPSPLPLAAGDPLPTESLMNSCLQARRKCOADPTCSAA 60
 QY 61 YHHLSDCTSSISTPLSEEPSVPADCLEAAQQLRNSLLIGCMCHRMKNQVACLDIYTV 120
 DB 61 YHHLSDCTSSISTPLSEEPSVPADCLEAAQQLRNSLLIGCMCHRMKNQVACLDIYTV 120
 QY 121 HPARSIGNVELDVSPYEDVTTSKPWKMLSKLMMKPDSDCLCKFAMLCITLNDKCDRLK 180
 DB 121 HPARSIGNVELDVSPYEDVTTSKPWKMLSKLMMKPDSDCLCKFAMLCITLNDKCDRLK 180
 QY 181 AYGEACSGPHCORHVCLQLLTFFKAAEPHQAQGLLLCPAPNDRGCGRRRTIAPNCA 240
 DB 181 AYGEACSGPHCORHVCLQLLTFFKAAEPHQAQGLLLCPAPNDRGCGRRRTIAPNCA 240
 QY 241 LPPVAPNCLLELRRLCFSDPLCRSLRVDFTQTHCPMDILGTCAEQSRCLRAVYLGIGTAM 300
 DB 241 LPPVAPNCLLELRRLCFSDPLCRSLRVDFTQTHCPMDILGTCAEQSRCLRAVYLGIGTAM 300
 QY 301 TENFVSNVNTSVALSCTCRGSGNLQECCEMLEGFSHNPCLTEATAAKRHFHSQSFQDW 360
 DB 301 TENFVSNVNTSVALSCTCRGSGNLQECCEMLEGFSHNPCLTEATAAKRHFHSQSFQDW 360
 QY 361 PHPTFAVMAHQENPAVRPQWPVPSLFCSTLPLILLLSLW 400
 DB 361 PHPTFAVMAHQENPAVRPQWPVPSLFCSTLPLILLLSLW 400
 RESULT 8
 AAB24411
 ID AAB24411 standard; protein; 400 AA.
 XX AC AAB24411;
 XX 07-NOV-2000 (first entry)
 XX Human PRO538 protein sequence SEQ ID NO:132.
 KW Human; PRO; promotion; inhibition; angiogenesis; cardiovascularisation;
 KW diagnosis; trauma; wound; cancer; atherosclerosis; cardiac hypertrophy;
 KW angiogenic; proliferative; cardiant; cardiovascular; antiatherosclerotic;
 KW cytostatic; gene therapy; vaccine.
 XX Homo sapiens.
 XX WO200032221-A2.
 XX 08-JUN-2000.
 XX 30-NOV-1999; 99WO-US028313.
 XX 01-DEC-1998; 98WO-US025108.
 XX 16-DEC-1998; 98US-0112850P.
 XX 12-JAN-1999; 99US-011554P.
 XX 08-MAR-1999; 99WO-US005028.
 XX 12-MAR-1999; 99US-0123957P.
 XX 28-APR-1999; 99US-0131445P.
 XX 14-MAY-1999; 99US-0134287P.
 XX 02-JUN-1999; 99WO-US012252.
 XX 23-JUN-1999; 99US-0141037P.
 XX 20-JUL-1999; 99US-0144758P.
 XX 26-JUL-1999; 99US-0145698P.
 XX 01-SEP-1999; 99WO-US020111.
 XX 08-SEP-1999; 99WO-US020594.
 XX 13-SEP-1999; 99WO-US020944.
 XX 15-SEP-1999; 99WO-US021090.
 XX 15-SEP-1999; 99WO-US021547.
 XX 05-OCT-1999; 99WO-US023089.
 XX 23-OCT-1999; 99US-0162506P.
 XX (GETH) GENENTECH INC.
 PA

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XX Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Hillan KJ;
PI Goddard AJ, Godowski PJ, Gurney AL, Klein RD, Kuo SS, Paoni NF;
PI Smith V, Watanabe CK, Williams PM, Wood WI;
XX WPI; 2000-412154/35.
DR N-PSDB; AAA77617.
XX
XX Nucleic acids encoding PRO polypeptides useful for preventing, diagnosing
PT and treating diagnosing a cardiovascular, endothelial or angiogenic
PT disorders in mammals.
XX
XX Claim 72; Fig 48; 315pp; English.
XX
XX The present invention describes nucleic acids encoding PRO polypeptides
CC useful for preventing, diagnosing and treating diagnosing a
CC cardiovascular, endothelial or angiogenic disorder in mammals by
CC modulating cell proliferation, angiogenesis and cardiovascularisation,
CC and for identifying agonists and antagonists of these processes. The
CC nucleic acids and the proteins they encode may be used in the prevention,
CC treatment and diagnosis of diseases associated with inappropriate PRO
CC expression such as cardiovascular, endothelial or angiogenic disorders in
CC mammals (e.g. atherosclerosis, cancers and cardiac hypertrophy). For
CC example, the nucleic acids (NCs) and vectors containing them and the PRO
CC polypeptide may be used to treat disorders associated with decreased PRO
CC expression. AAA77510 to AAA77721 and AAB24388 to AAB24435 represent
CC nucleotide and protein sequences used in the exemplification of the
CC present invention
XX
XX Sequence 400 AA;
SQ
Query Match 100.0%; Score 2190; DB 3; Length 400;
Best Local Similarity 100.0%; Pred. No. 1.5e-193;
Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MVRPLNRPPLPPVVLMLLLLPSPPLAAGDPLPTESRLMNSCLQARRKQADPTCSAA 60
DB 1 MVRPLNRPPLPPVVLMLLLLPSPPLAAGDPLPTESRLMNSCLQARRKQADPTCSAA 60
QY 61 YHLDSTCTSSITPLPSEEPSVPADCLAAQQLRNSSLIGCMCHRRMKNQVACLDIYWTV 120
DB 61 YHLDSTCTSSITPLPSEEPSVPADCLAAQQLRNSSLIGCMCHRRMKNQVACLDIYWTV 120
QY 121 HRARSLGNYELDVSPYEDTTSKPKMNLKSLNMLKPDSDCLKFKAMLCITLNDKCDRLK 180
DB 121 HRARSLGNYELDVSPYEDTTSKPKMNLKSLNMLKPDSDCLKFKAMLCITLNDKCDRLK 180
QY 181 AYGEACSGPHCQHVCLRQLLTTFEKAABPHQAQGLLLCPCAPNDRGCGRRRNTIAPNCA 240
DB 181 AYGEACSGPHCQHVCLRQLLTTFEKAABPHQAQGLLLCPCAPNDRGCGRRRNTIAPNCA 240
QY 241 LPPVAPNCLERLRCFSDPLCRSLRVDFQTHCHPMDILGTCATEQSRCLRAYLGLGTAM 300
DB 241 LPPVAPNCLERLRCFSDPLCRSLRVDFQTHCHPMDILGTCATEQSRCLRAYLGLGTAM 300
QY 301 TPNFVSNVNTSVALSCTCRSGNMQECEMLEGFFSHNPCLTEAIAAKMFHSLQFSQDW 360
DB 301 TPNFVSNVNTSVALSCTCRSGNMQECEMLEGFFSHNPCLTEAIAAKMFHSLQFSQDW 360
QY 361 PHPTFAVMAHQNENPAVRPQWPVPSLPSTPLILLLSLW 400
DB 361 PHPTFAVMAHQNENPAVRPQWPVPSLPSTPLILLLSLW 400
RESULT 9
AAB00171
ID AAB00171 standard; protein; 400 AA.
XX
XX AAB00171;
AC
XX
XX 08-FEB-2001 (first entry)
XX
XX PRO538 polypeptide.

```

```

XX PRO211; PRO228; PRO538; PRO172; PRO182; neoplasia; inhibition; tumour;
KW treatment; therapy; agonist; antibody; breast cancer; ovarian cancer;
KW renal cancer; colorectal cancer; uterine cancer; prostate cancer;
KW lung cancer; bladder cancer; melanoma; leukaemia; inflammatory disorder;
KW angiogenic disorder; immunologic disorder; human.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Peptide 1..26
XX Modified-site /label= Signal peptide
XX Modified-site /note= "N-glycosylation site"
XX Modified-site 134..138
XX Modified-site /note= "Casein kinase II phosphorylation site"
XX Modified-site 148..152
XX Modified-site /note= "N-glycosylation site"
XX Modified-site 170..174
XX Modified-site /note= "Casein kinase II phosphorylation site"
XX Modified-site 202..206
XX Modified-site /note= "Casein kinase II phosphorylation site"
XX Modified-site 231..235
XX Modified-site /note= "cAMP- and cGMP-dependent protein kinase phosphorylation site"
XX Modified-site 279..285
XX Modified-site /note= "N-myristoylation site"
XX Modified-site 294..300
XX Binding-site /note= "N-myristoylation site"
XX Binding-site 306..317
XX Binding-site /label= Prokaryotic membrane lipoprotein lipid attachment site
XX Modified-site 309..313
XX Domain /note= "N-glycosylation site"
XX Binding-site 379..395
XX Binding-site /label= Transmembrane domain
XX Binding-site 379..390
XX Binding-site /label= Prokaryotic membrane lipoprotein lipid attachment site
XX WO200055319-A1.
XX
XX 21-SEP-2000.
XX
XX 02-DEC-1999; 99WO-US028564.
XX
XX 12-MAR-1999; 99US-0123957P.
XX 28-APR-1999; 99US-0131445P.
XX 20-JUL-1999; 99US-0144758P.
XX 26-JUL-1999; 99US-0145698P.
XX 08-SEP-1999; 99WO-US020594.
XX 15-SEP-1999; 99WO-US021090.
XX 05-OCT-1999; 99WO-US023089.
XX 30-NOV-1999; 99WO-US028313.
XX
XX (GETH ) GENENTECH INC.
XX
XX Ashkenazi AJ, Goddard A, Gurney AL, Klein RD, Napier MA, Wood WI;
XX Yuan J;
XX
XX WPI; 2000-638201/61.
XX N-PSDB; AAA54101.
XX
XX PRO211, PRO228, PRO538, PRO172 and PRO182 polypeptides useful for
PT treating tumors including cancers of the breast and lung, leukemia and
PT for identifying compounds capable of inhibiting growth of neoplastic
PT cells.
XX
XX Claim 31; Fig 6; 133pp; English.
XX
XX Isolated PRO211, PRO228, PRO538, PRO172 or PRO182 polypeptides or their
CC agonists (preferably anti-PRO agonist antibody or a small molecule
CC mimicking the biological activity of PRO polypeptide) are useful in vitro

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or in vivo for inhibiting the growth of a tumour cell. Compositions comprising the PRO polypeptides are useful for inhibiting neoplastic cell growth and for treating cancer including breast, ovarian, renal, colorectal, uterine, prostate, lung, bladder, central nervous system cancer, melanoma and leukaemia in a mammal. The PRO polypeptides are also useful for treating other disorders such as neuronal, glial, astrocytal, hypothalamic and other glandular, macrophagal, epithelial, stromal, blastocoele disorders and inflammatory, angiogenic and immunologic disorders as well as being useful for identifying agonists to PRO polypeptides by contacting the polypeptide with a candidate molecule and monitoring biological activity mediated by the polypeptide

Sequence 400 AA;

Query Match 100.0%; Score 2190; DB 3; Length 400;
 Best Local Similarity 100.0%; Pred. No. 1.5e-193;
 Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVRPLNRPPLPPVVLMLLLPSPPLAAGDPLPTESLMNSCLQARRKQADPTCSAA 60
 DB 1 MVRPLNRPPLPPVVLMLLLPSPPLAAGDPLPTESLMNSCLQARRKQADPTCSAA 60

QY 61 YHLDSCSTSSISTPLPSPSPVPADCLEAAQQLRNSLLGCMCHRRMKQVACLDIYWTV 120
 DB 61 YHLDSCSTSSISTPLPSPSPVPADCLEAAQQLRNSLLGCMCHRRMKQVACLDIYWTV 120

QY 121 HRARSLGNELVSPYEDVTTSKPKWKNLSKLNMLKPDSDCLKPFAMLTCLNDKCDRLRK 180
 DB 121 HRARSLGNELVSPYEDVTTSKPKWKNLSKLNMLKPDSDCLKPFAMLTCLNDKCDRLRK 180

QY 181 AYGEACSGPHCORHVCLRLQLTFFKAAEPHAGLLCPAPNDRCGGRRNTIAPNCA 240
 DB 181 AYGEACSGPHCORHVCLRLQLTFFKAAEPHAGLLCPAPNDRCGGRRNTIAPNCA 240

QY 241 LPPVAPNCLERLRCFSDPLCRSLVDFTQCHPMDILGTCAEQSRCLRAYLGLIGTAM 300
 DB 241 LPPVAPNCLERLRCFSDPLCRSLVDFTQCHPMDILGTCAEQSRCLRAYLGLIGTAM 300

QY 301 TPNFVSNVNTSVALSCTCRSGNLQECMELEGFFSHNPFCLTEIAAKRFRHSQFSQDW 360
 DB 301 TPNFVSNVNTSVALSCTCRSGNLQECMELEGFFSHNPFCLTEIAAKRFRHSQFSQDW 360

QY 361 PHPTFAVMAHONENPAVRPOPWPVPSLFSCTLPILLLSLW 400
 DB 361 PHPTFAVMAHONENPAVRPOPWPVPSLFSCTLPILLLSLW 400

RESULT 10

ID AAB24050 standard; protein; 400 AA.

AC AAB24050;

DT 25-JAN-2001 (first entry)

DE Human PRO538 protein sequence SEQ ID NO:20.

Human; tumour; diagnosis; neoplastic disease; identification; cancer; tumorigenesis; detection; neoplastic cell growth; proliferation; cytostatic; antiinflammatory; immunomodulatory; inflammatory disorder; immunological disorder.

OS Homo sapiens.

XX WO200053754-A1.

XX 14-SEP-2000.

XX 06-JAN-2000; 2000WO-US000277.

XX 08-MAR-1999; 99WO-US0005028.

XX 12-MAR-1999; 99US-0123957P.

XX 29-MAR-1999; 99US-0126773P.

PR 21-APR-1999; 99US-0130232P.
 PR 28-APR-1999; 99US-0131445P.
 PR 05-OCT-1999; 99WO-US023089.
 PR 30-NOV-1999; 99WO-US028313.
 PR 02-DEC-1999; 99WO-US028551.
 PR 02-DEC-1999; 99WO-US028564.
 PR 30-DEC-1999; 99WO-US031243.
 PR 30-DEC-1999; 99WO-US031274.
 XX (GETH) GENENTECH INC.
 PA Baker KP, Desauvage FJ, Goddard A, Gurney AL, Klein RD, Roy MA;
 XX Wood WI;
 PI WPI; 2000-572269/53.
 DR N-PSDB; AAC58234.
 XX New isolated antibody for use in compositions and methods for the
 PT diagnosis and treatment of neoplastic cell growth and proliferation in
 PT mammals, including humans, and in monitoring tumor treatment.
 XX Claim 61; Fig 20; 195pp; English.

The present invention describes an isolated antibody (Ab) that binds to one of the human proteins (P) designated PRO213, PRO1330, PRO1449, PRO237, PRO324, PRO351, PRO362, PRO615, PRO331, PRO338, PRO3664, PRO618, PRO772, PRO703, PRO792 or PRO474. The Ab can be used in compositions and methods for the diagnosis and treatment of neoplastic cell growth and proliferation in mammals, including humans. Genes and polypeptides encoded by them, that are amplified in the genome of a tumour cell, can be identified and are useful targets for the treatment and prevention of certain cancers and may be used to monitor tumour treatment. Compounds that inhibit the expression or activity of the identified polypeptides can be identified and used as antagonists. Benign or malignant tumours, inflammatory disorders and immunological disorders can be treated. AAC58123 to AAC58224 represent hybridisation probes and PCR primers used in the isolation of the human PRO sequences. AAC58225 to AAC58241 and AAC24041 to AAC24056 represent human PRO polynucleotide and protein sequences given in the exemplification of the present invention

Sequence 400 AA;

Query Match 100.0%; Score 2190; DB 3; Length 400;
 Best Local Similarity 100.0%; Pred. No. 1.5e-193;
 Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVRPLNRPPLPPVVLMLLLPSPPLAAGDPLPTESLMNSCLQARRKQADPTCSAA 60
 DB 1 MVRPLNRPPLPPVVLMLLLPSPPLAAGDPLPTESLMNSCLQARRKQADPTCSAA 60

QY 61 YHLDSCSTSSISTPLPSPSPVPADCLEAAQQLRNSLLGCMCHRRMKQVACLDIYWTV 120
 DB 61 YHLDSCSTSSISTPLPSPSPVPADCLEAAQQLRNSLLGCMCHRRMKQVACLDIYWTV 120

QY 121 HRARSLGNELVSPYEDVTTSKPKWKNLSKLNMLKPDSDCLKPFAMLTCLNDKCDRLRK 180
 DB 121 HRARSLGNELVSPYEDVTTSKPKWKNLSKLNMLKPDSDCLKPFAMLTCLNDKCDRLRK 180

QY 181 AYGEACSGPHCORHVCLRLQLTFFKAAEPHAGLLCPAPNDRCGGRRNTIAPNCA 240
 DB 181 AYGEACSGPHCORHVCLRLQLTFFKAAEPHAGLLCPAPNDRCGGRRNTIAPNCA 240

QY 241 LPPVAPNCLERLRCFSDPLCRSLVDFTQCHPMDILGTCAEQSRCLRAYLGLIGTAM 300
 DB 241 LPPVAPNCLERLRCFSDPLCRSLVDFTQCHPMDILGTCAEQSRCLRAYLGLIGTAM 300

QY 301 TPNFVSNVNTSVALSCTCRSGNLQECMELEGFFSHNPFCLTEIAAKRFRHSQFSQDW 360
 DB 301 TPNFVSNVNTSVALSCTCRSGNLQECMELEGFFSHNPFCLTEIAAKRFRHSQFSQDW 360

QY 361 PHPTFAVMAHONENPAVRPOPWPVPSLFSCTLPILLLSLW 400
 DB 361 PHPTFAVMAHONENPAVRPOPWPVPSLFSCTLPILLLSLW 400

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RESULT 11
ADJ58713
ID ADJ58713 standard; protein; 400 AA.
XX
AC ADJ58713;
XX
DT 06-MAY-2004 (first entry)
XX
DE Human retL3 protein.
XX
KW Tissue growth; retL protein; organ failure; foetal malformation;
KW tumour growth; renal tissue; cytostatic; vulnery; nephrotropic; human.
XX
OS Homo sapiens.
XX
PN US6677135-B1.
XX
PD 13-JAN-2004.
XX
PF 06-NOV-1998; 98US-00187906.
XX
PR 08-MAY-1996; 96US-0017427P.
PR 07-JUN-1996; 96US-0019300P.
PR 16-JUL-1996; 96US-0021859P.
PR 23-AUG-1996; 96US-0023444P.
PR 11-APR-1997; 97US-0043533P.
PR 07-MAY-1997; 97WO-US007726.
XX
PA (BIOJ ) BIOGEN INC.
XX
PI Sanicola-Nadel M, Hession C, Cate RL, Worley DS;
XX
WPI: 2004-079845/08.
DR N-PSDB; ADJ58712.
XX
New nucleic acid encoding Ret polypeptide, useful for diagnosing and/or
PT treating diseases or conditions associated with aberrant expression or
PT activity of the Ret ligand, such as organ failure, fetal malformations
PT and tumor growth.
XX
PS Claim 1; SEQ ID NO 21; 66pp; English.
XX
CC The present invention relates to nucleotide and amino acid sequences
CC which promote tissue growth and methods for modulating tissue growth. The
CC invention also relates to retL proteins and polynucleotides encoding such
CC proteins. RetL proteins interact with a receptor protein Ret to trigger
CC dimerisation and/or autophosphorylation of the tyrosine kinase domain of
CC the receptor protein Ret. The methods and compositions of the present
CC invention are useful for the diagnosis and/or treatment of diseases or
CC conditions associated with aberrant expression or activity of the Ret
CC ligand, such as organ failure, foetal malformations and tumour growth and
CC for promoting regeneration or survival of damaged renal tissue. The
CC present sequence is human retL3 protein of the invention.
XX
SQ Sequence 400 AA;

Query Match 100.0%; Score 2190; DB 8; Length 400;
Best Local Similarity 100.0%; Pred. No. 1.5e-193;
Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVRPLNRPPLPPVVLMLLLPSPPLAAGDPLPTESRLMNSCLQARRKQADPTCSAA 60
DB 1 MVRPLNRPPLPPVVLMLLLPSPPLAAGDPLPTESRLMNSCLQARRKQADPTCSAA 60
QY 61 YHLDSCSTSSITPLPSEPSVPADCLEAAQQLRNSLIGCMCHRRMKQVACLDIYWTV 120
DB 61 YHLDSCSTSSITPLPSEPSVPADCLEAAQQLRNSLIGCMCHRRMKQVACLDIYWTV 120
QY 121 HRARSLGNVELDVSPYEDVTTSKPKWNLKLNKLPKSDCLKFMALCTLNDKCDRLRK 180
DB 121 HRARSLGNVELDVSPYEDVTTSKPKWNLKLNKLPKSDCLKFMALCTLNDKCDRLRK 180

181 AYGEACSGPHCQRHVCLRLQLLTFFEKAAEPHAQGLLPCAPNDRGCGERRNTIAPNCA 240
181 AYGEACSGPHCQRHVCLRLQLLTFFEKAAEPHAQGLLPCAPNDRGCGERRNTIAPNCA 240
241 LPPVAPNCLRLCLFSDPLCRSRLVDFQTHCHPMDILGTCAEQSRCLRAYLGLIGTAM 300
241 LPPVAPNCLRLCLFSDPLCRSRLVDFQTHCHPMDILGTCAEQSRCLRAYLGLIGTAM 300
301 TPNFVSNVNTSVALSCTCRSGNQLQECCEMLEGFFSHNPCLTETAIARAKMRFHLSQSDW 360
301 TPNFVSNVNTSVALSCTCRSGNQLQECCEMLEGFFSHNPCLTETAIARAKMRFHLSQSDW 360
361 PHPTFAVMAHQENPAVRPQWPVPSLFSCTPLILLISLW 400
361 PHPTFAVMAHQENPAVRPQWPVPSLFSCTPLILLISLW 400

RESULT 12
ADT94302
ID ADT94302 standard; protein; 400 AA.
XX
AC ADT94302;
XX
DT 16-DEC-2004 (first entry)
XX
DE Human PRO538 protein.
XX
KW cytostatic; ophthalmological; cardiant; vulnery; angiogenesis inhibitor;
KW angiogenesis stimulator; cardiovascular; gene therapy; diagnosis;
KW mutation; cardiovascular disorder; endothelial disorder;
KW angiogenic disorder; myocardial infarction; cardiac hypertrophy; trauma;
KW cancer; macular degeneration; PGF2alpha; primary angioplasty.
XX
OS Homo sapiens.
XX
PN AU2003259607-A1.
XX
PD 27-NOV-2003.
XX
PF 31-OCT-2003; 2003AU-00259607.
XX
PR 30-NOV-1999; 2000AU-00017482.
XX
(GETH ) GENENTECH INC.
XX
PI Williams PM, Watanabe CK, Smith V, Paoni NF, Kuo SS, Klein RD;
PI Gurney AL, Godowski PJ, Goddard A, Hillan KJ, Gerber H, Ferrara N;
PI Baker KP, Ashkenazi AJ, Wood WI;
XX
WPI: 2004-662630/65.
DR N-PSDB; ADT94301.
XX
Diagnosing disease e.g. cardiovascular, endothelial or angiogenic
PT disorder in mammal, related to mutation in PRO1303 polypeptide-encoding
PT nucleic acid sequence, by determining presence or absence of mutation in
PT nucleic acid sequence.
XX
Example 27; SEQ ID NO 132; 301pp; English.
XX
The invention relates to a method of diagnosing (M1) a disease or
CC susceptibility to a disease which is related to a mutation in a PRO1303
CC polypeptide-encoding nucleic acid sequence, by determining the presence
CC or absence of the mutation in the polypeptide-encoding nucleic acid
CC sequence, where the presence or absence of the mutation is indicative of
CC the presence or absence of the disease or susceptibility to the disease.
CC The method is useful for diagnosing a disease or angiogenic disorder in a
CC disease e.g. cardiovascular, endothelial or angiogenic disorder in a
CC mammal. The method is also useful for treating a cardiovascular,
CC endothelial or angiogenic disorder in a mammal, especially human. The
CC human has suffered myocardial infarction. The human has cardiac
CC hypertrophy, trauma, a cancer or age-related macular degeneration. The
CC cardiac hypertrophy is characterized by the presence of an elevated level

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CC of PGF2alpha. The PRO1303 polypeptide is administered together with a
CC cardiovascular, endothelial or angiogenic agent. The PRO-1303 polypeptide
CC is administered following primary angioplasty. The cardiovascular,
CC endothelial or angiogenic disorder is cancer. The method is useful for
CC inhibiting endothelial cell growth in a mammal. The method is further
CC useful for stimulating endothelial cell growth in a mammal. The PRO1303
CC nucleic acid molecule or polypeptide is useful in the manufacture of a
CC medicament for treating or diagnosing a cardiovascular, endothelial or
CC angiogenic disorder in a mammal. The medicament is for treating humans.
CC This sequence corresponds to a PRO protein of the invention.

XX SQ Sequence 400 AA;

Query Match 100.0%; Score 2190; DB 8; Length 400;
Best Local Similarity 100.0%; Pred. No. 1.5e-193;
Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVRPLNRPPLPVVLMMLLLPPSPPLAAGDPLPTESLMNSCLQARRKCOADPTCSAA 60
DB 1 MVRPLNRPPLPVVLMMLLLPPSPPLAAGDPLPTESLMNSCLQARRKCOADPTCSAA 60
QY 61 YHHLDSCTSSISTPLPSEPSVPADCLEAAQQLRNSSLIGCMCHRRMKQVACLDIYWTV 120
DB 61 YHHLDSCTSSISTPLPSEPSVPADCLEAAQQLRNSSLIGCMCHRRMKQVACLDIYWTV 120
QY 121 HRARSLGNVELDVSPYEDVTTSKPKWNLKLNMLKPDSDCLCKFAMLCCTLNDKCDRLRK 180
DB 121 HRARSLGNVELDVSPYEDVTTSKPKWNLKLNMLKPDSDCLCKFAMLCCTLNDKCDRLRK 180
QY 181 AYGEACSGPHCORHVCLRLQLTFFFEKAAEPHAQGLLLCPCAPNDRCGERRNTIAPNCA 240
DB 181 AYGEACSGPHCORHVCLRLQLTFFFEKAAEPHAQGLLLCPCAPNDRCGERRNTIAPNCA 240
QY 241 LPPVAPNCLRLRCLFSDPLCRSLVDFQTHCHPMDILGTCAEQSRCLRAYLGLIGTAM 300
DB 241 LPPVAPNCLRLRCLFSDPLCRSLVDFQTHCHPMDILGTCAEQSRCLRAYLGLIGTAM 300
QY 301 TENFVSNVNTSVALSCTCRSGNLOECCEMLEGFFSHNPFCLTEATAAKMRFHSQSFQDW 360
DB 301 TENFVSNVNTSVALSCTCRSGNLOECCEMLEGFFSHNPFCLTEATAAKMRFHSQSFQDW 360
QY 361 PHPTFAVMAHQENPAVRPQWPVPSLFCSTLPLILLLSLW 400
DB 361 PHPTFAVMAHQENPAVRPQWPVPSLFCSTLPLILLLSLW 400

RESULT 13
ADY53849

ID ADY53849 standard; protein; 400 AA.

XX AC ADY53849;

XX DT 05-MAY-2005 (first entry)

XX DE Human retL3 protein.

XX KW DNA purification; immune stimulation; ret ligand.

XX OS Homo sapiens.

XX PN US6861509-B1.

XX PD 01-MAR-2005.

XX PF 21-JAN-2000; 2000US-00489407.

XX PR 08-MAY-1996; 96US-0017427P.

XX PR 07-JUN-1996; 96US-0019300P.

XX PR 16-JUL-1996; 96US-0021859P.

XX PR 23-AUG-1996; 96US-0023444P.

XX PR 11-APR-1997; 97US-0043533P.

XX PR 07-MAY-1997; 97WO-US007726.

XX PR 06-NOV-1998; 98US-00187906.

XX

PA (BIOJ) BIOGEN INC.

XX PI Sanicola-Nadel M, Hession C, Cate RL, Worley DS;

XX DR WPI; 2005-201184/21.

XX DR N-PSDB; ADY53848.

XX PT New anti-Ret ligand (RetL) antibody, useful for treating acute renal
PT failure, acute nephritis, chronic renal failure, nephrotic syndrome, as
PT well as Alzheimer's disease, Parkinson's and multiple sclerosis.

XX PS Disclosure; SEQ ID NO 21; 66pp; English.

XX CC The invention relates to an antibody produced by a hybridoma selected
CC from the group consisting of AA.F99 and AA.GE7.3. The antibody is used to
CC stimulate neural and renal cell growth. This sequence corresponds to a
CC protein sequence of the invention.

XX SQ Sequence 400 AA;

Query Match 100.0%; Score 2190; DB 9; Length 400;
Best Local Similarity 100.0%; Pred. No. 1.5e-193;
Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVRPLNRPPLPVVLMMLLLPPSPPLAAGDPLPTESLMNSCLQARRKCOADPTCSAA 60

DB 1 MVRPLNRPPLPVVLMMLLLPPSPPLAAGDPLPTESLMNSCLQARRKCOADPTCSAA 60

QY 61 YHHLDSCTSSISTPLPSEPSVPADCLEAAQQLRNSSLIGCMCHRRMKQVACLDIYWTV 120

DB 61 YHHLDSCTSSISTPLPSEPSVPADCLEAAQQLRNSSLIGCMCHRRMKQVACLDIYWTV 120

QY 121 HRARSLGNVELDVSPYEDVTTSKPKWNLKLNMLKPDSDCLCKFAMLCCTLNDKCDRLRK 180

DB 121 HRARSLGNVELDVSPYEDVTTSKPKWNLKLNMLKPDSDCLCKFAMLCCTLNDKCDRLRK 180

QY 181 AYGEACSGPHCORHVCLRLQLTFFFEKAAEPHAQGLLLCPCAPNDRCGERRNTIAPNCA 240

DB 181 AYGEACSGPHCORHVCLRLQLTFFFEKAAEPHAQGLLLCPCAPNDRCGERRNTIAPNCA 240

QY 241 LPPVAPNCLRLRCLFSDPLCRSLVDFQTHCHPMDILGTCAEQSRCLRAYLGLIGTAM 300

DB 241 LPPVAPNCLRLRCLFSDPLCRSLVDFQTHCHPMDILGTCAEQSRCLRAYLGLIGTAM 300

QY 301 TENFVSNVNTSVALSCTCRSGNLOECCEMLEGFFSHNPFCLTEATAAKMRFHSQSFQDW 360

DB 301 TENFVSNVNTSVALSCTCRSGNLOECCEMLEGFFSHNPFCLTEATAAKMRFHSQSFQDW 360

QY 361 PHPTFAVMAHQENPAVRPQWPVPSLFCSTLPLILLLSLW 400

DB 361 PHPTFAVMAHQENPAVRPQWPVPSLFCSTLPLILLLSLW 400

RESULT 14

ADZ00213

ID ADZ00213 standard; protein; 400 AA.

XX AC ADZ00213;

XX DT 30-JUN-2005 (first entry)

XX DE Human Ret ligand 3 (RetL3), SEQ ID NO:21.

XX KW Cell growth; development; signal transduction; neurological disease;
KW renal disease; genitourinary disease; neuroprotective; nephrotropic;
KW cancer; neoplasm; cytostatic; RetL3;

XX KW Ret tyrosine kinase receptor ligand 3; Ret ligand 3;

XX KW GDNF family receptor alpha 3; GFR3.

XX OS Homo sapiens.

XX PN US2005080235-A1.

XX PD 14-APR-2005.
 XX PF 23-SEP-2003; 2003US-00668936.
 XX PR 08-MAY-1996; 96US-0017427P.
 XX PR 07-JUN-1996; 96US-0019300P.
 XX PR 16-JUL-1996; 96US-0021859P.
 XX PR 23-AUG-1996; 96US-0023444P.
 XX PR 11-APR-1997; 97US-0043533P.
 XX PR 07-MAY-1997; 97MO-US007726.
 XX PR 06-NOV-1998; 98US-00187906.
 XX (SANI/) SANICOLA-NADEL M.
 PA (HESS/) HESSION C.
 PA (CATE/) CATE R L.
 PA (WORL/) WORLEY D S.
 XX Sanicola-Nadel M, Hession C, Cate RL, Worley DS;
 XX WPI; 2005-305025/31.
 XX N-PSDB; AD200212.
 XX
 PT New polypeptide sequence that interacts with a receptor protein Ret to
 PT trigger dimerization or autophosphorylation, useful in preparing a
 PT composition for treating neurodegenerative disorders, e.g., Alzheimer's
 PT disease.
 XX
 PS Claim 1; SEQ ID NO 21; 67pp; English.
 XX
 CC The invention relates to the murine and human RetL3 (Ret ligand 3)
 CC proteins (AD200209 and AD200213, respectively) and to proteins at least
 CC 80% identical to murine or human RetL3. The invention also discloses
 CC other RetL3 proteins such as rat RetL1, human RetL1, human RetL2,
 CC fragments of human RetL1, mouse RetL3, and human RetL3, and cDNA sequences
 CC encoding these RetL3 proteins or protein fragments. Like other RetL
 CC proteins, the RetL3 proteins of the invention interact with the Ret
 CC receptor tyrosine kinase that is encoded by the Ret proto-oncogene,
 CC triggering Ret receptor dimerization or autophosphorylation. The Ret
 CC receptor is expressed during development in a variety of tissues,
 CC including the peripheral and central nervous systems and the kidney. It
 CC is also expressed in some cancers. RetL proteins such as the murine and
 CC human RetL3 proteins, and RetL polynucleotides may be used for
 CC stimulating Ret receptor signaling, thereby promoting renal or neuronal
 CC cell growth or survival and minimizing damage to such tissues after
 CC various insults. They may therefore be used to treat renal disorders
 CC (e.g., renal failure, renal tube defects and renal trauma) or
 CC neurological disorders including neurodegenerative disorders (e.g.,
 CC Alzheimer's disease), bacterial or viral diseases of the nervous system
 CC (e.g., meningitis), neurological damage (e.g. that caused by hemorrhage
 CC or trauma) and developmental neural disorders (e.g., mental retardation).
 CC Conversely, antibodies against RetL may be used to block RetL-Ret
 CC receptor signal transduction for inhibiting tumor growth, fusion proteins
 CC comprising a RetL protein are useful for targeting a drug to Ret receptor
 CC -expressing tumors. Anti-RetL antibodies and RetL fusion proteins may
 CC also be used in medical imaging. The present sequence represents a
 CC specifically claimed full-length human RetL3 protein encoded by cDNA
 CC isolated in the invention.
 XX
 SQ Sequence 400 AA;
 Query Match 100.0%; Score 2190; DB 9; Length 400;
 Best Local Similarity 100.0%; Pred. No. 1.5e-193;
 Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MVRPLNRPPLPPVVMILLPLPSPLPLAAGDPLPTESRLMNSCLQARRKQADPTCSAA 60
 DB 1 MVRPLNRPPLPPVVMILLPLPSPLPLAAGDPLPTESRLMNSCLQARRKQADPTCSAA 60
 QY 61 YHLDSCSTSSITPLPSEPSVPADCLAAQQLNSLIGCMCHRRMKNQVACLDIYWTY 120
 DB 61 YHLDSCSTSSITPLPSEPSVPADCLAAQQLNSLIGCMCHRRMKNQVACLDIYWTY 120

QY 121 HRARSLGNVELDVSPYEDTIVTSKPKWKNLSKLNMLKPDSDLCKFAMLCITLNDKCDRLRK 180
 DB 121 HRARSLGNVELDVSPYEDTIVTSKPKWKNLSKLNMLKPDSDLCKFAMLCITLNDKCDRLRK 180
 QY 181 AYGEACSGPHCORHVCLROLLTFPEKAAEPHAQGLLIPCAPNDRGCGERRNTIAPNCA 240
 DB 181 AYGEACSGPHCORHVCLROLLTFPEKAAEPHAQGLLIPCAPNDRGCGERRNTIAPNCA 240
 QY 241 LPPVAPNCLRLRCLCFSDPLCRSLRVLDFQTHCHPMDILGTCAEQSCLRAYLGLIGTAM 300
 DB 241 LPPVAPNCLRLRCLCFSDPLCRSLRVLDFQTHCHPMDILGTCAEQSCLRAYLGLIGTAM 300
 QY 301 TPNFVSNVNTSVALSCTCRSGNLQEECEMLEGFFSHNPCLTEAIAAMRPHSOLFQSDW 360
 DB 301 TPNFVSNVNTSVALSCTCRSGNLQEECEMLEGFFSHNPCLTEAIAAMRPHSOLFQSDW 360
 QY 361 PHPTFAVMAHONENPAVRPQWPVPSLPSCTPLILLISLW 400
 DB 361 PHPTFAVMAHONENPAVRPQWPVPSLPSCTPLILLISLW 400
 RESULT 15
 AAY15179
 ID AAY15179 standard; protein; 628 AA.
 XX AC AAY15179;
 XX DT 07-FEB-2000 (first entry)
 XX DE GFRalpha3-IgG fusion protein.
 XX KW GFRalpha3-IgG fusion protein; recombinant expression; epitope tag;
 KW Baculovirus-infected insect cell; Baculovirus expression vector;
 KW restriction enzyme; subcloning; GFRalpha3 ligand; GFRalpha3;
 KW glial-cell-line-derived neurotrophic factor family receptor alpha-3;
 KW peripheral nervous system disease; autonomic nervous system dysfunction.
 XX OS Homo sapiens.
 XX OS Synthetic.
 XX PN WO9949039-A2.
 XX PD 30-SEP-1999.
 XX PF 19-MAR-1999; 99WO-US006098.
 XX PR 23-MAR-1998; 98US-0079124P.
 XX PR 13-APR-1998; 98US-0081569P.
 XX (GETH) GENENTECH INC.
 XX PI De Sauvage FJ, Klein RD, Phillips HS, Rosenthal A;
 XX WPI; 2000-038358/03.
 XX New isolated GFR-alpha3 nucleic acid, used to develop products for
 XX treating diseases or conditions involving peripheral nervous system or
 XX autonomic nervous system.
 XX Example 8; Page 101-104; 112pp; English.
 XX The present sequence is GFRalpha3-IgG fusion protein. This was used for
 XX recombinant expression of GFRalpha3 in Baculovirus-infected insect cells.
 XX The GFRalpha3 was fused upstream of an epitope tag contained within a
 XX Baculovirus expression vector. The product was digested with selected
 XX restriction enzymes and subcloned into the expression vector. This fusion
 XX was also used to determine GFRalpha3 binding. GFRalpha3
 XX ligands can be useful in the treatment of peripheral nervous system
 XX diseases and autonomic nervous system dysfunctions
 XX SQ Sequence 628 AA;
 Query Match 100.0%; Score 2190; DB 3; Length 628;

Best Local Similarity 100.0%; Pred. No. 2.7e-193;
Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MVRPLNRPPLPPVVLMLLLPSPPLAAGDPLPTESRLMNSCLQARRKQADPTCSAA	60
Db	1	MVRPLNRPPLPPVVLMLLLPSPPLAAGDPLPTESRLMNSCLQARRKQADPTCSAA	60
Qy	61	YHLDSTSSISTPLPSEPSVPADCLEAAQQLRNSSLIGCMCHRRMKNOVACLDIYWTV	120
Db	61	YHLDSTSSISTPLPSEPSVPADCLEAAQQLRNSSLIGCMCHRRMKNOVACLDIYWTV	120
Qy	121	HRARSLGNVELDVSPYEDVTTSKPMXNLSKLNMLKPDSDCLKPFAMLCTLNDKCDRLRK	180
Db	121	HRARSLGNVELDVSPYEDVTTSKPMXNLSKLNMLKPDSDCLKPFAMLCTLNDKCDRLRK	180
Qy	181	AYGEACSGPHCQHVCLRQLLTFFEKAAEPHAQGLLLCPCAPNDRGCGERRNTIAPNCA	240
Db	181	AYGEACSGPHCQHVCLRQLLTFFEKAAEPHAQGLLLCPCAPNDRGCGERRNTIAPNCA	240
Qy	241	LPPVAPNCLERELCFSDPLCRSRLVDFQTHCHPMDILGTCATEQSRLRAYLGLIGTAM	300
Db	241	LPPVAPNCLERELCFSDPLCRSRLVDFQTHCHPMDILGTCATEQSRLRAYLGLIGTAM	300
Qy	301	TPNFVSNVNTSVALSCTCRSGNLQECMELEGFFSHNPCLTEAIAAKMRFHSOLFSDW	360
Db	301	TPNFVSNVNTSVALSCTCRSGNLQECMELEGFFSHNPCLTEAIAAKMRFHSOLFSDW	360
Qy	361	PHPTFAVMAHQENPAVRQPWPVPSLFSCTPLILLLSLW	400
Db	361	PHPTFAVMAHQENPAVRQPWPVPSLFSCTPLILLLSLW	400

Search completed: May 12, 2006, 02:04:18
Job time : 145.527 secs

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 12, 2006, 02:10:01 ; Search time 33.6261 Seconds
(without alignments)
983.470 Million cell updates/sec

Title: US-10-668-936-21

Perfect score: 2190

Sequence: 1 MVRPLNRPPLPPVLMMLL.....PWVPSLFCSTPLILLLSLW 400

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: /cgn2_6/ptodata/1/iaa/5_COMB.pep.*
- 2: /cgn2_6/ptodata/1/iaa/6_COMB.pep.*
- 3: /cgn2_6/ptodata/1/iaa/H_COMB.pep.*
- 4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2190	100.0	400	2	US-09-220-528-63
2	2190	100.0	400	2	US-09-187-906-21
3	2190	100.0	400	2	US-09-949-016-9079
4	2190	100.0	400	2	US-09-489-407-21
5	1708	78.0	315	2	US-09-187-906-19
6	1708	78.0	315	2	US-09-489-407-19
7	1646.5	75.2	397	2	US-09-220-528-64
8	1646.5	75.2	397	2	US-09-187-906-17
9	1646.5	75.2	397	2	US-09-489-407-17
10	1455	66.4	346	2	US-09-187-906-15
11	1455	66.4	346	2	US-09-489-407-15
12	542.5	24.8	445	2	US-08-861-990-11
13	542.5	24.8	464	2	US-08-957-063-6
14	542.5	24.8	464	2	US-09-487-685-6
15	542.5	24.8	464	2	US-08-802-805D-6
16	542.5	24.8	464	2	US-08-861-990-2
17	542.5	24.8	464	2	US-09-388-316C-6
18	542.5	24.8	664	2	US-08-957-063-18
19	542.5	24.8	664	2	US-09-487-685-18
20	542.5	24.8	664	2	US-08-802-805D-18
21	542.5	24.8	664	2	US-09-388-316C-18
22	540.5	24.7	464	2	US-08-957-063-3
23	540.5	24.7	464	2	US-09-487-685-3
24	540.5	24.7	464	2	US-08-802-805D-3
25	540.5	24.7	464	2	US-09-187-906-13
26	540.5	24.7	464	2	US-08-861-990-9
27	540.5	24.7	464	2	US-09-388-316C-3

28	540.5	24.7	464	2	US-09-489-407-13	Sequence 13, Appl
29	540.5	24.7	664	2	US-08-957-063-16	Sequence 16, Appl
30	540.5	24.7	664	2	US-09-487-685-16	Sequence 16, Appl
31	540.5	24.7	664	2	US-08-802-805D-16	Sequence 16, Appl
32	540.5	24.7	664	2	US-09-388-316C-16	Sequence 16, Appl
33	517.5	23.6	460	2	US-08-802-805D-22	Sequence 22, Appl
34	517.5	23.6	460	2	US-09-187-906-11	Sequence 11, Appl
35	517.5	23.6	460	2	US-09-489-407-11	Sequence 11, Appl
36	516	23.6	463	2	US-08-837-199A-10	Sequence 10, Appl
37	516	23.6	463	2	US-08-837-199A-12	Sequence 12, Appl
38	516	23.6	465	2	US-08-837-199A-2	Sequence 2, Appl
39	516	23.6	465	2	US-08-861-990-8	Sequence 8, Appl
40	516	23.6	465	2	US-09-388-316C-22	Sequence 22, Appl
41	515	23.5	465	2	US-08-837-199A-6	Sequence 6, Appl
42	511	23.3	468	2	US-08-802-805D-21	Sequence 21, Appl
43	511	23.3	468	2	US-08-837-199A-4	Sequence 4, Appl
44	511	23.3	468	2	US-08-860-370-2	Sequence 2, Appl
45	511	23.3	468	2	US-09-187-906-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1

US-09-220-528-63
; Sequence 63, Application US/09220528A
; Patent No. 6284540
; GENERAL INFORMATION:
; APPLICANT: Milbrandt, Jeffrey D.
; APPLICANT: Baloh, Robert H.
; TITLE OF INVENTION: Artemin, A No. 6284540el Neurotrophic Factor
; FILE REFERENCE: 6029-7998
; CURRENT APPLICATION NUMBER: US/09/220,528A
; CURRENT FILING DATE: 1998-12-24
; EARLIER APPLICATION NUMBER: 09/218,698
; EARLIER FILING DATE: 1998-12-22
; EARLIER APPLICATION NUMBER: 60/108,148
; EARLIER FILING DATE: 1998-11-12
; EARLIER APPLICATION NUMBER: 09/163,283
; EARLIER FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 120
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 63
; LENGTH: 400
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-220-528-63

Query Match	100.0%;	Score 2190;	DB 2;	Length 400;
Best Local Similarity	100.0%;	Pred. No. 4.6e-207;		
Matches	400;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;
QY	1	MVRPLNRPPLPPVLMMLLLPPSPPLAAGDPLPTESRLMNSCLQARRKCOADPTCSAA	60	
Db	1	MVRPLNRPPLPPVLMMLLLPPSPPLAAGDPLPTESRLMNSCLQARRKCOADPTCSAA	60	
QY	61	YHLDSCSTSSISITPLSEEPSVPADCLEAAQOLRNSLLIGCMCHRRKMQVACLDIYWTV	120	
Db	61	YHLDSCSTSSISITPLSEEPSVPADCLEAAQOLRNSLLIGCMCHRRKMQVACLDIYWTV	120	
QY	121	HRARSLGNVELDVSPYEDVTTSKPMQNLKSNMLKPDSDCLKFMALCTLNDKCDRLRK	180	
Db	121	HRARSLGNVELDVSPYEDVTTSKPMQNLKSNMLKPDSDCLKFMALCTLNDKCDRLRK	180	
QY	181	AYGEACSGPHCBQHVCLRQLLTFFEKAAEPHAGLLICPCAPNDRCGGERRNTIAPNCA	240	
Db	181	AYGEACSGPHCBQHVCLRQLLTFFEKAAEPHAGLLICPCAPNDRCGGERRNTIAPNCA	240	
QY	241	LPPVAPNCLERRLCFSDPLCRSLVDFTQCHPMDILGTCAEQSKRLRAYLGLGTAM	300	
Db	241	LPPVAPNCLERRLCFSDPLCRSLVDFTQCHPMDILGTCAEQSKRLRAYLGLGTAM	300	
QY	301	TPNFVSNVNTSVALSCTCRGSGNLQBECEMLEGFFSHNFCPLTEAIAAKRHFHSQDWF	360	

Db 301 TPNFVSNVNTSVALSCTCRGSGNLQECCEMLEGFFSHNFCPLTEATAAKRHFHSQSFQDM 360
QY 361 PHTFAVMAHQENPAVRPQPWPVPSLFSCTPLPILLLSLW 400
Db 361 PHTFAVMAHQENPAVRPQPWPVPSLFSCTPLPILLLSLW 400
RESULT 2
US-09-187-906-21
; Sequence 21, Application US/09187906
; Patent No. 6677135
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC.
; TITLE OF INVENTION: Ret Ligand (RetL) for Stimulating Neural
; TITLE OF INVENTION: and Renal Growth
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Biogen, Inc.
; STREET: 14 Cambridge Center
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02142
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/187,906
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/07726
; FILING DATE: 07-MAY-97
; APPLICATION NUMBER: US 60/017,427
; FILING DATE: 08-MAY-96
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/019,300
; FILING DATE: 07-JUN-96
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/021,859
; FILING DATE: 16-JUL-96
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/043,533
; FILING DATE: 10-APR-97
; ATTORNEY/AGENT INFORMATION:
; NAME: Kaplan, Warren A.
; REGISTRATION NUMBER: 34,199
; REFERENCE/DOCKET NUMBER: A008 PCT CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-679-2400
; TELEFAX: 617-679-2838
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 400 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-187-906-21
Query Match 100.0%; Score 2190; DB 2; Length 400;
Best Local Similarity 100.0%; Pred. No. 4.6e-207;
Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MVRPLNRPPLPPVVLMLLLPSPPLAAGDPLPTESRLMNSCLQARRKCOADPTCSAA 60
Db 1 MVRPLNRPPLPPVVLMLLLPSPPLAAGDPLPTESRLMNSCLQARRKCOADPTCSAA 60
QY 61 YHLDSTSSISTPLPSEEPSVPADCLEAAQQLRNSLIGCMCHRRMKNQVACLDIYWTV 120
Db 61 YHLDSTSSISTPLPSEEPSVPADCLEAAQQLRNSLIGCMCHRRMKNQVACLDIYWTV 120
QY 61 YHLDSTSSISTPLPSEEPSVPADCLEAAQQLRNSLIGCMCHRRMKNQVACLDIYWTV 120
Db 61 YHLDSTSSISTPLPSEEPSVPADCLEAAQQLRNSLIGCMCHRRMKNQVACLDIYWTV 120

QY 121 HRASIGNVELDVSPYEDVTTSKPMKMLSKLNMKPSDSDLCLEFAMLTCLNDKCDRLRK 180
Db 121 HRASIGNVELDVSPYEDVTTSKPMKMLSKLNMKPSDSDLCLEFAMLTCLNDKCDRLRK 180
QY 181 AYGEACSGPHCORHVCLRQLLTFFPKAAEPHAQGLLLCPCAPNDRGCGERRRNTIAPNCA 240
Db 181 AYGEACSGPHCORHVCLRQLLTFFPKAAEPHAQGLLLCPCAPNDRGCGERRRNTIAPNCA 240
QY 241 LPPVAPNCLERLRCFSDPLCRSLVDFQTHCHPMDILGTCAEQSRCLRAYLIGLGTAM 300
Db 241 LPPVAPNCLERLRCFSDPLCRSLVDFQTHCHPMDILGTCAEQSRCLRAYLIGLGTAM 300
QY 301 TPNFVSNVNTSVALSCTCRGSGNLQECCEMLEGFFSHNFCPLTEATAAKRHFHSQSFQDM 360
Db 301 TPNFVSNVNTSVALSCTCRGSGNLQECCEMLEGFFSHNFCPLTEATAAKRHFHSQSFQDM 360
QY 361 PHTFAVMAHQENPAVRPQPWPVPSLFSCTPLPILLLSLW 400
Db 361 PHTFAVMAHQENPAVRPQPWPVPSLFSCTPLPILLLSLW 400
RESULT 3
US-09-949-016-9079
; Sequence 9079, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9079
; LENGTH: 400
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-9079
Query Match 100.0%; Score 2190; DB 2; Length 400;
Best Local Similarity 100.0%; Pred. No. 4.6e-207;
Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MVRPLNRPPLPPVVLMLLLPSPPLAAGDPLPTESRLMNSCLQARRKCOADPTCSAA 60
Db 1 MVRPLNRPPLPPVVLMLLLPSPPLAAGDPLPTESRLMNSCLQARRKCOADPTCSAA 60
QY 61 YHLDSTSSISTPLPSEEPSVPADCLEAAQQLRNSLIGCMCHRRMKNQVACLDIYWTV 120
Db 61 YHLDSTSSISTPLPSEEPSVPADCLEAAQQLRNSLIGCMCHRRMKNQVACLDIYWTV 120
QY 121 HRASIGNVELDVSPYEDVTTSKPMKMLSKLNMKPSDSDLCLEFAMLTCLNDKCDRLRK 180
Db 121 HRASIGNVELDVSPYEDVTTSKPMKMLSKLNMKPSDSDLCLEFAMLTCLNDKCDRLRK 180
QY 181 AYGEACSGPHCORHVCLRQLLTFFPKAAEPHAQGLLLCPCAPNDRGCGERRRNTIAPNCA 240
Db 181 AYGEACSGPHCORHVCLRQLLTFFPKAAEPHAQGLLLCPCAPNDRGCGERRRNTIAPNCA 240
QY 241 LPPVAPNCLERLRCFSDPLCRSLVDFQTHCHPMDILGTCAEQSRCLRAYLIGLGTAM 300
Db 241 LPPVAPNCLERLRCFSDPLCRSLVDFQTHCHPMDILGTCAEQSRCLRAYLIGLGTAM 300
QY 301 TPNFVSNVNTSVALSCTCRGSGNLQECCEMLEGFFSHNFCPLTEATAAKRHFHSQSFQDM 360
Db 301 TPNFVSNVNTSVALSCTCRGSGNLQECCEMLEGFFSHNFCPLTEATAAKRHFHSQSFQDM 360

Db 301 TPNFVSNVNTSVALSCTCRSGNLOECEMLEGFFSHNPCLTEIAIAAKMRHFSOLFQSDW 360
 Qy 361 PHPTFAVMAHONENPAVRPQPWVPSLFSCTPLILLISLW 400
 Db 361 PHPTFAVMAHONENPAVRPQPWVPSLFSCTPLILLISLW 400

RESULT 4

US-09-489-407-21
 ; Sequence 21, Application US/09489407
 ; Patent No. 6861509

GENERAL INFORMATION:

APPLICANT: BIOGEN, INC.

TITLE OF INVENTION: Ret Ligand (RetL) for Stimulating Neural

TITLE OF INVENTION: and Renal Growth

NUMBER OF SEQUENCES: 21

CORRESPONDENCE ADDRESS:

ADDRESSEE: Biogen, Inc.

STREET: 14 Cambridge Center

CITY: Cambridge

STATE: MA

COUNTRY: USA

ZIP: 02142

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/489,407

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US97/07726

FILING DATE: 07-MAY-97

APPLICATION NUMBER: US 60/017,427

FILING DATE: 08-MAY-96

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/019,300

FILING DATE: 07-JUN-96

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/021,859

FILING DATE: 16-JUL-96

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/043,533

FILING DATE: 10-APR-97

ATTORNEY/AGENT INFORMATION:

NAME: Kaplan, Warren A.

REGISTRATION NUMBER: 34,199

REFERENCE/DOCKET NUMBER: A008 PCT CIP

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-679-2400

TELEFAX: 617-679-2838

INFORMATION FOR SEQ ID NO: 21:

SEQUENCE CHARACTERISTICS:

LENGTH: 400 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-489-407-21

Query Match 100.0%; Score 2190; DB 2; Length 400;
 Best Local Similarity 100.0%; Pred. No. 4.6e-207;
 Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MVRPLNRPPLPPVVMILLPLPSPLPLAAGDPLPESRLMNSCLQARRKQADPTCSAA 60

Db 1 MVRPLNRPPLPPVVMILLPLPSPLPLAAGDPLPESRLMNSCLQARRKQADPTCSAA 60

Qy 61 YHLDSCSTSSISPLPSEEPSVPADCLAAQAQLRNSSLIGCMCHRRMKNQVACLDIYWTY 120

Db 61 YHLDSCSTSSISPLPSEEPSVPADCLAAQAQLRNSSLIGCMCHRRMKNQVACLDIYWTY 120

Qy 121 HRARSLGNELDYSPYEDTIVTSKPWKMLSKLNMKLPDSCLCKFAMLCFLNDKCDRLRK 180
 Db 121 HRARSLGNELDYSPYEDTIVTSKPWKMLSKLNMKLPDSCLCKFAMLCFLNDKCDRLRK 180
 Qy 181 AYGEACSGPHCORHVCLROLLTFPEKAAEPHAQGLLLCPCAPNDRGCGERRNTIAPNCA 240
 Db 181 AYGEACSGPHCORHVCLROLLTFPEKAAEPHAQGLLLCPCAPNDRGCGERRNTIAPNCA 240
 Qy 241 LPPVAPNCLRLCFSDPLCRSRLVDFQTHCPMDILGTCAEQSRCLRAYLGLIGTAM 300
 Db 241 LPPVAPNCLRLCFSDPLCRSRLVDFQTHCPMDILGTCAEQSRCLRAYLGLIGTAM 300
 Qy 301 TPNFVSNVNTSVALSCTCRSGNLOECEMLEGFFSHNPCLTEIAIAAKMRHFSOLFQSDW 360
 Db 301 TPNFVSNVNTSVALSCTCRSGNLOECEMLEGFFSHNPCLTEIAIAAKMRHFSOLFQSDW 360
 Qy 361 PHPTFAVMAHONENPAVRPQPWVPSLFSCTPLILLISLW 400
 Db 361 PHPTFAVMAHONENPAVRPQPWVPSLFSCTPLILLISLW 400

RESULT 5

US-09-187-906-19

; Sequence 19, Application US/09187906

; Patent No. 6677135

GENERAL INFORMATION:

APPLICANT: BIOGEN, INC.

TITLE OF INVENTION: Ret Ligand (RetL) for Stimulating Neural

TITLE OF INVENTION: and Renal Growth

NUMBER OF SEQUENCES: 21

CORRESPONDENCE ADDRESS:

ADDRESSEE: Biogen, Inc.

STREET: 14 Cambridge Center

CITY: Cambridge

STATE: MA

COUNTRY: USA

ZIP: 02142

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/187,906

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US97/07726

FILING DATE: 07-MAY-97

APPLICATION NUMBER: US 60/017,427

FILING DATE: 08-MAY-96

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/019,300

FILING DATE: 07-JUN-96

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/021,859

FILING DATE: 16-JUL-96

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/043,533

FILING DATE: 10-APR-97

ATTORNEY/AGENT INFORMATION:

NAME: Kaplan, Warren A.

REGISTRATION NUMBER: 34,199

REFERENCE/DOCKET NUMBER: A008 PCT CIP

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-679-2400

TELEFAX: 617-679-2838

INFORMATION FOR SEQ ID NO: 19:

SEQUENCE CHARACTERISTICS:

LENGTH: 315 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-187-906-19

Query Match 78.0%; Score 1708; DB 2; Length 315;
Best Local Similarity 100.0%; Pred. No. 9.3e-160;
Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 92 QLRNSSLIGCMCHRRMKNQVACLDIYWTVHRARSLGNVELDVSYPEDTTSKPWKNLK 151
DB 7 QLRNSSLIGCMCHRRMKNQVACLDIYWTVHRARSLGNVELDVSYPEDTTSKPWKNLK 66
QY 152 LNMKPDSDCLKFAMLCTLNDCDRLRKAYGACSGPHCORHVCLRLQLLTFEKAAPH 211
DB 67 LNMKPDSDCLKFAMLCTLNDCDRLRKAYGACSGPHCORHVCLRLQLLTFEKAAPH 126
QY 212 AQGLLPCAPNDRGCGERRNTIAPNCALPPVAPNCLRLCFSDPLCRSLVDFOFH 271
DB 127 AQGLLPCAPNDRGCGERRNTIAPNCALPPVAPNCLRLCFSDPLCRSLVDFOFH 186
QY 272 CHPMDILGTCAEQSRCLRAYLGLIGTAMTPNFVSNVNTSVALSCTCRSGNLQBECEML 331
DB 187 CHPMDILGTCAEQSRCLRAYLGLIGTAMTPNFVSNVNTSVALSCTCRSGNLQBECEML 246
QY 332 EGFSSHNPCLTEAIAAKRHFHLSQFSDQWPHPTFAVMAHONENPAVRPOPWVPSLFSCTL 391
DB 247 EGFSSHNPCLTEAIAAKRHFHLSQFSDQWPHPTFAVMAHONENPAVRPOPWVPSLFSCTL 306
QY 392 PLILLSLW 400
DB 307 PLILLSLW 315

RESULT 6

US-09-489-407-19
Sequence 19, Application US/09489407
Patent No. 6861509
GENERAL INFORMATION:
APPLICANT: BIOGEN, INC.
TITLE OF INVENTION: Ret Ligand (RetL) for Stimulating Neural
TITLE OF INVENTION: and Renal Growth
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Biogen, Inc.
STREET: 14 Cambridge Center
CITY: Cambridge
STATE: MA
COUNTRY: USA
ZIP: 02142
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/489,407
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/07726
FILING DATE: 07-MAY-97
APPLICATION NUMBER: US 60/017,427
FILING DATE: 08-MAY-96
PRIOR APPLICATION DATA: US 60/019,300
APPLICATION NUMBER: US 60/019,300
FILING DATE: 07-JUN-96
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/021,859
FILING DATE: 16-JUL-96
PRIOR APPLICATION DATA: US 60/043,533
APPLICATION NUMBER: US 60/043,533
FILING DATE: 10-APR-97
ATTORNEY/AGENT INFORMATION:
NAME: Kaplan, Warren A.
REGISTRATION NUMBER: 34,199

REFERENCE/DOCKET NUMBER: A008 PCT CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-679-2400
TELEFAX: 617-679-2838
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 315 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-489-407-19

Query Match 78.0%; Score 1708; DB 2; Length 315;
Best Local Similarity 100.0%; Pred. No. 9.3e-160;
Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 92 QLRNSSLIGCMCHRRMKNQVACLDIYWTVHRARSLGNVELDVSYPEDTTSKPWKNLK 151
DB 7 QLRNSSLIGCMCHRRMKNQVACLDIYWTVHRARSLGNVELDVSYPEDTTSKPWKNLK 66
QY 152 LNMKPDSDCLKFAMLCTLNDCDRLRKAYGACSGPHCORHVCLRLQLLTFEKAAPH 211
DB 67 LNMKPDSDCLKFAMLCTLNDCDRLRKAYGACSGPHCORHVCLRLQLLTFEKAAPH 126
QY 212 AQGLLPCAPNDRGCGERRNTIAPNCALPPVAPNCLRLCFSDPLCRSLVDFOFH 271
DB 127 AQGLLPCAPNDRGCGERRNTIAPNCALPPVAPNCLRLCFSDPLCRSLVDFOFH 186
QY 272 CHPMDILGTCAEQSRCLRAYLGLIGTAMTPNFVSNVNTSVALSCTCRSGNLQBECEML 331
DB 187 CHPMDILGTCAEQSRCLRAYLGLIGTAMTPNFVSNVNTSVALSCTCRSGNLQBECEML 246
QY 332 EGFSSHNPCLTEAIAAKRHFHLSQFSDQWPHPTFAVMAHONENPAVRPOPWVPSLFSCTL 391
DB 247 EGFSSHNPCLTEAIAAKRHFHLSQFSDQWPHPTFAVMAHONENPAVRPOPWVPSLFSCTL 306
QY 392 PLILLSLW 400
DB 307 PLILLSLW 315

RESULT 7

US-09-220-528-64
Sequence 64, Application US/09220528A
Patent No. 6284540
GENERAL INFORMATION:
APPLICANT: Milbrandt, Jeffrey D.
TITLE OF INVENTION: Artemin, A No. 6284540e1 Neurotrophic Factor
FILE REFERENCE: 6029-7998
CURRENT APPLICATION NUMBER: US/09/220,528A
CURRENT FILING DATE: 1998-12-24
EARLIER APPLICATION NUMBER: 09/218,698
EARLIER FILING DATE: 1998-12-22
EARLIER APPLICATION NUMBER: 60/108,148
EARLIER FILING DATE: 1998-11-12
EARLIER APPLICATION NUMBER: 09/163,283
EARLIER FILING DATE: 1998-09-29
NUMBER OF SEQ ID NOS: 120
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 64
LENGTH: 397
TYPE: PRT
ORGANISM: Murine
US-09-220-528-64

Query Match 75.2%; Score 1646.5; DB 2; Length 397;
Best Local Similarity 77.8%; Pred. No. 1.5e-153;
Matches 305; Conservative 30; Mismatches 56; Indels 1; Gaps 1;
QY 9 PLPPVVMLLLLPSPFLAAGDPLPTESLMNSCLQARRKCOADPTCSAAYHLDSC 68
DB 7 PRPP-LLMILLVLSLWFLGAGNSLATENRFVNSCTQARKKEANPACKAAVOHLSCT 65

Qy 69 SSISTPLPSEPSVPADCLEAAQRLNSSLIGCMCHRMKNQVACLDIYTVHRAISLGN 128
Db 66 SLSRPLPLEBSAMSADCLEAAEQRLNSSLIDCRCHRMKHQATCLDIYTVHRAISLGD 125
Qy 129 YELDVSPYEDVTTSKPKWKNLSKLNMLKPDSDCLCFKAMLTNDKCDRLRKAYGEACSG 188
Db 126 YELDVSPYEDVTTSKPKWKNLSKLNMLKPDSDCLCFKAMLTNDKCDRLRKAYGEACSG 185
Qy 189 PHCORHVCRLQLTFFFEKAAEPHAQGLLLCPANDRGCGERRRNTIAPNCALPPVAPNC 248
Db 186 IRCORHLCLAQLRSFFFEKAAESHAQGLLLCPAPEDAGCGERRRNTIAPSCALPSVTPNC 245
Qy 249 LELRLCFSDPLCRSRLVDFQTHCHPMDIILGTCAEQSRCLRAYLGLIGTAMTNPFSNV 308
Db 246 LELRSPCRADPLCRSRLMDPQTHCHPMDIILGTCAEQSRCLRAYLGLIGTAMTNPFSKV 305
Qy 309 NTSVALSCTCRGSGNLQCECEMLEGFFSHNPCI TEAIAAKMRFHSQLFSDQWPHPTFVAVM 368
Db 306 NTVVALSCTCRGSGNLQCECEQLERSFSQNPCLVEAIAAKMRFHRLQFSQWADSTFSV 365
Qy 369 AHONENPAVRPQWPVPSLFSCTPLILLLSLW 400
Db 366 QQNSNPALRLQPLPLPSILPLILLQTLW 397

RESULT 8

US-09-187-906-17
; Sequence 17, Application US/09187906
; Patent No. 6671135
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC.
; TITLE OF INVENTION: Ret Ligand (RetL) for Stimulating Neural
; TITLE OF INVENTION: and Renal Growth
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Biogen, Inc.
; STREET: 14 Cambridge Center
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02142
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: US/09/187,906
; CLASSIFICATION:
; PRIOR APPLICATION DATA: PCT/US97/07726
; FILING DATE: 07-MAY-97
; APPLICATION NUMBER: US 60/017,427
; FILING DATE: 08-MAY-96
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/019,300
; FILING DATE: 07-JUN-96
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/021,859
; FILING DATE: 16-JUL-96
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/043,533
; FILING DATE: 10-APR-97
; ATTORNEY/AGENT INFORMATION:
; NAME: Kaplan, Warren A.
; REGISTRATION NUMBER: 34,199
; REFERENCE/DOCKET NUMBER: A008 PCT CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-679-2400
; TELEFAX: 617-679-2838
; INFORMATION FOR SEQ ID NO: 17:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 397 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-187-906-17

Query Match 75.2%; Score 1646.5; DB 2; Length 397;
Best Local Similarity 77.8%; Pred. No. 1.5e-153;
Matches 305; Conservative 30; Mismatches 56; Indels 1; Gaps 1;

Qy 9 PLPPVVMILLPLPPSPPLAAGDPLPESRLMNSCLQARRKQADPTCSAAVHHLDSCT 68
Db 7 PRPP-LIMILLVLSLWPLPLGAGNSLATENRFVNSCTQARKKCEANPACKAAVQHLGSC 65
Qy 69 SSISTPLPSEPSVPADCLEAAQRLNSSLIGCMCHRMKNQVACLDIYTVHRAISLGN 128
Db 66 SLSRPLPLEBSAMSADCLEAAEQRLNSSLIDCRCHRMKHQATCLDIYTVHRAISLGD 125
Qy 129 YELDVSPYEDVTTSKPKWKNLSKLNMLKPDSDCLCFKAMLTNDKCDRLRKAYGEACSG 188
Db 126 YELDVSPYEDVTTSKPKWKNLSKLNMLKPDSDCLCFKAMLTNDKCDRLRKAYGEACSG 185
Qy 189 PHCORHVCRLQLTFFFEKAAEPHAQGLLLCPANDRGCGERRRNTIAPNCALPPVAPNC 248
Db 186 IRCORHLCLAQLRSFFFEKAAESHAQGLLLCPAPEDAGCGERRRNTIAPSCALPSVTPNC 245
Qy 249 LELRLCFSDPLCRSRLVDFQTHCHPMDIILGTCAEQSRCLRAYLGLIGTAMTNPFSNV 308
Db 246 LELRSPCRADPLCRSRLMDPQTHCHPMDIILGTCAEQSRCLRAYLGLIGTAMTNPFSKV 305
Qy 309 NTSVALSCTCRGSGNLQCECEMLEGFFSHNPCI TEAIAAKMRFHSQLFSDQWPHPTFVAVM 368
Db 306 NTVVALSCTCRGSGNLQCECEQLERSFSQNPCLVEAIAAKMRFHRLQFSQWADSTFSV 365
Qy 369 AHONENPAVRPQWPVPSLFSCTPLILLLSLW 400
Db 366 QQNSNPALRLQPLPLPSILPLILLQTLW 397

RESULT 9
US-09-489-407-17
; Sequence 17, Application US/09489407
; Patent No. 6861509
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC.
; TITLE OF INVENTION: Ret Ligand (RetL) for Stimulating Neural
; TITLE OF INVENTION: and Renal Growth
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Biogen, Inc.
; STREET: 14 Cambridge Center
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02142
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/489,407
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/07726
; FILING DATE: 07-MAY-97
; APPLICATION NUMBER: US 60/017,427
; FILING DATE: 08-MAY-96
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/019,300
; FILING DATE: 07-JUN-96


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; PRIOR APPLICATION DATA: US 60/021,859
; APPLICATION NUMBER: US 60/021,859
; FILING DATE: 16-JUL-96
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/043,533
; FILING DATE: 10-APR-97
; ATTORNEY/AGENT INFORMATION:
; NAME: Kaplan, Warren A.
; REGISTRATION NUMBER: 34,199
; REFERENCE/DOCKET NUMBER: A008 PCT CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-679-2400
; TELEFAX: 617-679-2838
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 397 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-489-407-17

Query Match 75.2%; Score 1646.5; DB 2; Length 397;
Best Local Similarity 77.8%; Pred. No. 1.5e-153;
Matches 305; Conservative 30; Mismatches 56; Indels 1; Gaps 1;

QY 9 PLPPVLMILLPPSPPLAAGDPLPESRLMNSCLQARRKCOADPTCSAAVHLDSCST 68
DB 7 PRPP-LMILLVLSLWLPGLAGNSLATENRFVNSCTQARKCEANPACKAAAYOHLGSGT 65

QY 69 SSISTPLPSEPSVPADCLEAAQQLRNSSLIGCMCHRMKNQVACLDIYVTVHARSLSGN 128
DB 66 SLSRPLPLEESAMSDCLEAAQQLRNSSLIDCRCHRMKHQATCLDIYVTVHARSLSGD 125

QY 129 YELDVSPYEDTVTSKPMKNLSKLNMLKPDSDCLCKFAMLCCLNDKCDRLRKAYGEACSG 188
DB 126 YELDVSPYEDTVTSKPMKNLSKLNMLKPDSDCLCKFAMLCCLNDKCDRLRKAYGEACSG 185

QY 189 PHCORHVLRLQTLFFKAAEPHAQGLLLCPAPNDRGCGERRNTIAPNCALPPVAPNC 248
DB 186 IRCORHLCLAQLRSFFKAAESHAQGLLLCPAPEDAGCGERRNTIAPSCALPSVTPNC 245

QY 249 LELRLCFSDPLCRSLVDFQTHCHPMDILGTCTEQSRCLRAYLGLGTAMTPNFVSNV 308
DB 246 LDLSRCFADPLCRSLMDFTQTHCHPMDILGTCTEQSRCLRAYLGLGTAMTPNFISKV 305

QY 309 NTSVALSCTCRSGNLOECEMLEGFFSHNPCLTEAIAAKMRPHSQLFSDQWPHPTFAVM 368
DB 306 NTTVALSCTCRSGNLOECEQLERSFSQNPCLVEAIAAKMRPHRQLFSQDWDSTFSVV 365

QY 369 AHQENPAVRPQWPVPSLFSCTPLILLLSLW 400
DB 366 QQNSNPALRLQPRLPILSFSILPLLILLQTLW 397

RESULT 10
US-09-187-906-15
; Sequence 15, Application US/09187906
; Patent No. 6677135
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC.
; TITLE OF INVENTION: Ret Ligand (RetL) for Stimulating Neural
; TITLE OF INVENTION: and Renal Growth
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Biogen, Inc.
; STREET: 14 Cambridge Center
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02142
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/187,906
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/07726
; FILING DATE: 07-MAY-97
; APPLICATION NUMBER: US 60/017,427
; FILING DATE: 08-MAY-96
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/019,300
; FILING DATE: 07-JUN-96
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/021,859
; FILING DATE: 16-JUL-96
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/043,533
; FILING DATE: 10-APR-97
; ATTORNEY/AGENT INFORMATION:
; NAME: Kaplan, Warren A.
; REGISTRATION NUMBER: 34,199
; REFERENCE/DOCKET NUMBER: A008 PCT CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-679-2400
; TELEFAX: 617-679-2838
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 346 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-187-906-15

Query Match 66.4%; Score 1455; DB 2; Length 346;
Best Local Similarity 80.9%; Pred. No. 8.6e-135;
Matches 267; Conservative 21; Mismatches 42; Indels 0; Gaps 0;

QY 71 ISTPLPSEPSVPADCLEAAQQLRNSSLIGCMCHRMKNQVACLDIYVTVHARSLSGN 130
DB 17 LSRPLPLEESAMSDCLEAAQQLRNSSLIDCRCHRMKHQATCLDIYVTVHARSLSGD 76

QY 131 LDVSPYEDTVTSKPMKNLSKLNMLKPDSDCLCKFAMLCCLNDKCDRLRKAYGEACSGPH 190
DB 77 LDVSPYEDTVTSKPMKNLSKLNMLKPDSDCLCKFAMLCCLNDKCDRLRKAYGEACSGIR 136

QY 191 CORHVLRLQTLFFKAAEPHAQGLLLCPAPNDRGCGERRNTIAPNCALPPVAPNCLE 250
DB 137 CORHLCLAQLRSFFKAAESHAQGLLLCPAPEDAGCGERRNTIAPSCALPSVTPNCILD 196

QY 251 LRLCFSDPLCRSLVDFQTHCHPMDILGTCTEQSRCLRAYLGLGTAMTPNFVSNVNT 310
DB 197 LRSFCRADPLCRSLMDFTQTHCHPMDILGTCTEQSRCLRAYLGLGTAMTPNFISKVT 256

QY 311 SVALSCTCRSGNLOECEMLEGFFSHNPCLTEAIAAKMRPHSQLFSDQWPHPTFAVMAH 370
DB 257 TVALSCTCRSGNLOECEQLERSFSQNPCLVEAIAAKMRPHRQLFSQDWDSTFSVQQ 316

QY 371 QNENPAVRPQWPVPSLFSCTPLILLLSLW 400
DB 317 QNSNPALRLQPRLPILSFSILPLLILLQTLW 346

RESULT 11
US-09-489-407-15
; Sequence 15, Application US/09489407
; Patent No. 6861509
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC.
; TITLE OF INVENTION: Ret Ligand (RetL) for Stimulating Neural
; TITLE OF INVENTION: and Renal Growth
; NUMBER OF SEQUENCES: 21

```

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Biogen, Inc.
 STREET: 14 Cambridge Center
 CITY: Cambridge
 STATE: MA
 COUNTRY: USA
 ZIP: 02142
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/489,407
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA: PCT/US97/07726
 FILING DATE: 07-MAY-97
 APPLICATION NUMBER: US 60/017,427
 FILING DATE: 08-MAY-96
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/019,300
 FILING DATE: 07-JUN-96
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/021,859
 FILING DATE: 16-JUL-96
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/043,533
 FILING DATE: 10-APR-97
 ATTORNEY/AGENT INFORMATION:
 NAME: Kaplan, Warren A.
 REGISTRATION NUMBER: 34,199
 REFERENCE/DOCKET NUMBER: A008 PCT CIP
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-679-2400
 TELEFAX: 617-679-2838
 INFORMATION FOR SEQ ID NO: 15:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 346 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09-489-407-15

Query Match 66.4%; Score 1455; DB 2; Length 346;
 Best Local Similarity 80.9%; Pred. No. 8.6e-135;
 Matches 267; Conservative 21; Mismatches 42; Indels 0; Gaps 0;
 Qy 71 ISTPLPEEPSPVADCLAEAAQRLNSSLIGCMCHRRMKNQVACLDIYVTVHRAARSLGNYE 130
 Db 17 LSRPLPLEESAMSADCLAEAEQLRNSLIDCRCHRRMKHQATCLDIYVTVHRAARSLGNYE 76
 Qy 131 LDVSPYEDTTSKPKWKNLKLNLKPDSDLCLKPFAMLCNTLNKCDRLRKAYGEACSGPH 190
 Db 77 LDVSPYEDTTSKPKWKNLKLNLKPDSDLCLKPFAMLCNTLNKCDRLRKAYGEACSGIR 136
 Qy 191 CORHVCRLQLLTPEKAABHAQGLLILCPAPNDRCGERRNTIAPNCALPPVAPNCL 250
 Db 137 CORHLCUQLRSFPEKAABHAQGLLILCPAPNDRCGERRNTIAPNCALPPVAPNCL 196
 Qy 251 LRLCLFSDPLCRSLVDFTQCHPMDILGTCAEQSRCLRAYLGLIGTAMTPNFVSNVNT 310
 Db 197 LRSFCRADPLCRSLVDFTQCHPMDILGTCAEQSRCLRAYLGLIGTAMTPNFISKVNT 256
 Qy 311 SVALSCTCRSGNLOECEMELEGFFSHNPCLTEIAAANKGFHSQLFSQDWPHTFAWAH 370
 Db 257 TVALSCTCRSGNLOECEQLERSFSQNPCLVEIAAANKGFHSQLFSQDWDSTFVSVOQ 316
 Qy 371 QNENPAVRPOPWPSLFSCTLPILILSLW 400
 Db 317 QNSNPAURLQPRUPLFSILPLILQLTLW 346

RESULT 12
 US-08-861-990-11
 ; Sequence 11, Application US/08861990
 ; Patent No. 6696259
 ; GENERAL INFORMATION:
 ; APPLICANT: Ibanez, Carlos F.
 ; APPLICANT: Arumae, Urmas
 ; APPLICANT: Sariola, Hannu
 ; APPLICANT: Suvalto, Petro
 ; APPLICANT: Trupp, Miles
 ; APPLICANT: Saarna, Mart
 ; TITLE OF INVENTION: Glial Cell Line-Derived Neurotropic Factor Receptors
 ; FILE REFERENCE: CEPH0418
 ; CURRENT APPLICATION NUMBER: US/08/861,990
 ; CURRENT FILING DATE: 1997-05-22
 ; PRIOR APPLICATION NUMBER: 08/747,842
 ; PRIOR FILING DATE: 1996-11-13
 ; PRIOR APPLICATION NUMBER: 60/006,619
 ; PRIOR FILING DATE: 1995-11-13
 ; PRIOR APPLICATION NUMBER: 60/015,767
 ; PRIOR FILING DATE: 1996-04-16
 ; PRIOR APPLICATION NUMBER: 60/021,965
 ; PRIOR FILING DATE: 1996-06-27
 ; PRIOR APPLICATION NUMBER: 60/020,638
 ; PRIOR FILING DATE: 1996-06-27
 ; PRIOR APPLICATION NUMBER: 60/020,639
 ; PRIOR FILING DATE: 1996-06-27
 ; NUMBER OF SEQ ID NOS: 11
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 11
 ; LENGTH: 445
 ; TYPE: PRT
 ; ORGANISM: Rattus sp.
 US-08-861-990-11
 Query Match 24.8%; Score 542.5; DB 2; Length 445;
 Best Local Similarity 37.4%; Pred. No. 8.2e-45;
 Matches 123; Conservative 42; Mismatches 125; Indels 39; Gaps 10;
 Qy 44 CLQARRKCOADPTCSAAHYHLDSCS--SISTPLPEEPSPVADCLAEAAQRLNSSLIGC 101
 Db 40 CVRANELCAESNCSSRYRTLRCLAGRDNTWLANKE-----CQAALEVLESPLYDC 93
 Qy 102 MCHRRMKNQVACLDIYVTVHRAARSLGNYELDVSPYEDTTSKPKWKNLKLNLKML----- 155
 Db 94 RCKRGMKELQCLQIYWSIHGLGTEGEFVEASPYE-PVTSR-----LSDFRLASIFSG 147
 Qy 156 -----KPDSDLCLKPFAMLCNTLNKCDRLRKAYGEACS-----GPHCQRHVCRLQLLT 203
 Db 148 TGTDPVAVSTKSNHCLDAKACNLNDNCKLRSSYISICNREISPTERCNRRKCKALRQF 207
 Qy 204 FEKAAEPHAQGLLILCPAPNDRCGERRNTIAPNCAL-PPVAPNCLLELRCLFSDPLCR 262
 Db 208 FDRVPSEYTYRMLFCS--ODQCAERRQTILPSCSYEDKEKPNCLDLRLSLCTDHLCR 265
 Qy 263 SRLVDFTQCHP--MDILGTCAEQSRCLRAYLGLIGTAMTPNFVSNVNTSVALS--CTC 318
 Db 266 SRLADPHANCASRYRTITPCADNYQACLSGYAGMIGFDMTPNYVDSNPTGIVVSPWCNC 325
 Qy 319 RGSNGNLOECEMELEGFFSHNPCLTEIAA 347
 Db 326 RGSNGNMEEBCEKFLRDTFENPCLRNAIOA 354

RESULT 13
 US-08-957-063-6
 ; Sequence 6, Application US/08957063
 ; Patent No. 6025157
 ; GENERAL INFORMATION:
 ; APPLICANT: Robert D. Klein, Arnon Rosenthal, Mary A. Hynes
 ; TITLE OF INVENTION: Neurturin Receptor
 ; NUMBER OF SEQUENCES: 19

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GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 12, 2006, 01:59:25 ; Search time 139.473 Seconds
(without alignments)
1250.660 Million cell updates/sec

Title: US-10-668-936-17
Perfect score: 2131
Sequence: 1 MGLSWSPRPPLMLLLVLS.....PRLPILSFLPILLQLTLW 397

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: Geneseqp1980s.*
2: Geneseqp1990s.*
3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003as.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*
9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2131	100.0	397	2 AAW37461	Aaw37461 Mouse Ret
2	2131	100.0	397	3 AAY84591	Aay84591 Amino aci
3	2131	100.0	397	3 AAY15174	Aay15174 Murine GF
4	2131	100.0	397	8 ADJ58709	Adj58709 Murine re
5	2131	100.0	397	9 ADY53845	Ady53845 Mouse ret
6	2131	100.0	397	9 ADZ00209	Adz00209 Mouse Ret
7	1972	92.5	397	2 AAW84182	Aaw84182 A GDNFR-a
8	1880	88.2	388	3 AAY15182	Aay15182 gd-GFRalp
9	1774	83.2	346	2 AAW37465	Aaw37465 Mouse Ret
10	1774	83.2	346	8 ADJ58707	Adj58707 Murine re
11	1774	83.2	346	8 ADY53843	Ady53843 Partial m
12	1774	83.2	346	9 ADZ00207	Adz00207 Mouse Ret
13	1646.5	77.3	400	2 AAW65116	Aaw65116 Human GDN
14	1646.5	77.3	400	2 AAW37463	Aaw37463 Human Ret
15	1646.5	77.3	400	2 AAW84186	Aaw84186 Glial cel
16	1646.5	77.3	400	3 AAY83226	Aay83226 PRO538 Po
17	1646.5	77.3	400	3 AAY84590	Aay84590 Amino aci
18	1646.5	77.3	400	3 AAY15177	Aay15177 Human GFR
19	1646.5	77.3	400	3 AAB19582	Aab19582 Human PRO
20	1646.5	77.3	400	3 AAB24411	Aab24411 Human PRO
21	1646.5	77.3	400	3 AAB00171	Aab00171 PRO538 po
22	1646.5	77.3	400	3 AAB24050	Aab24050 Human PRO
23	1646.5	77.3	400	8 ADJ58713	Adj58713 Human ret
24	1646.5	77.3	400	8 ADT94302	Adt94302 Human PRO

25	1646.5	77.3	400	9 ADY53849	Ady53849 Human ret
26	1646.5	77.3	400	9 ADZ00213	Adz00213 Human Ret
27	1646.5	77.3	628	3 AAY15179	Aay15179 GFRalphi3
28	1642.5	77.1	400	2 AAW84180	Aaw84180 A GDNFR-a
29	1640.5	77.0	400	2 AAW85117	Aaw85117 Human GDN
30	1531.5	71.9	378	2 AAW84185	Aaw84185 Glial cel
31	1458	68.4	369	3 AAY15178	Aay15178 Human GFR
32	1458	68.4	369	3 AAB19583	Aab19583 Human PRO
33	1458	68.4	369	3 AAB24051	Aab24051 Human PRO
34	1413	66.3	366	9 AEA39229	Aea39229 GRAL-rela
35	1386	65.0	315	2 AAW37462	Aaw37462 Human Ret
36	1386	65.0	315	8 ADJ58711	Adj58711 Human Ret
37	1386	65.0	315	9 ADY53847	Ady53847 Partial h
38	1386	65.0	315	9 ADZ00211	Adz00211 Human Ret
39	722	33.9	172	2 AAW65118	Aaw65118 Human GDN
40	654	30.7	498	2 AAW84183	Aaw84183 Consensus
41	640.5	30.1	489	2 AAW84298	Aaw84298 Consensus
42	577.5	27.1	460	2 AAW84181	Aaw84181 A GDNFR-a
43	577.5	27.1	464	2 AAW71602	Aaw71602 Rat neut
44	577.5	27.1	464	2 AAW92299	Aaw92299 Rat GDNFR
45	577.5	27.1	464	3 AAY80122	Aay80122 Rat neut

ALIGNMENTS

RESULT 1
AAW37461
ID AAW37461 standard; protein; 397 AA.
XX AC AAW37461;
XX
DT 21-MAY-1998 (first entry)
XX
DE Mouse Ret ligand RetL3.
XX
KW Ret ligand; RetL; RetL3; receptor; signal transduction; mouse;
KW cell growth; renal cell; nerve cell; renal failure; nephritis;
KW kidney transplant; toxic injury; hypoxic injury; neurodegeneration;
KW motor neurone disease; multiple sclerosis; infection; meningitis;
KW myelopathy; Croutfeldt-Jakob disease; cranial nerve injury;
KW spinal cord injury; Down's syndrome; cerebral palsy; Lyme disease;
KW muscular dystrophy; myasthenia gravis; tumour; therapy.
XX
OS Mus musculus.
XX
PN WO9744356-A2.
XX
PD 27-NOV-1997.
XX
PF 07-MAY-1997; 97WO-US007726.
XX
PR 08-MAY-1996; 96US-0017427P.
PR 07-JUN-1996; 96US-0019300P.
PR 16-JUL-1996; 96US-0021859P.
PR 11-APR-1997; 97US-0043533P.
XX
(BIOJ) BIOGEN INC.
XX
PI Sanicola-Nadel M, Hession C, Cate RL;
XX
DR WPI; 1998-018431/02.
XX
N-PSDB; AAV00249.
XX
PT New nucleic acid encoding ret receptor ligands and related proteins -
PT vectors, transformed cells and antibodies, used for promoting cell growth
PT and improving survival of injured cells, especially renal or nerve cells.
PS Claim 2; Page 77-78; 113pp; English.
XX
CC This amino acid sequence comprises mouse Ret ligand (RetL), deduced
CC from cDNA clones (see AAV00249) isolated from an EST database and by
CC 5'RACE. Rat and human RetL1, human RetL2 and RetL3 sequences (see

CC AAW37457-60 and AAW37462-63) are also claimed, RetL is a key component of
CC the Ret signalling pathway that specifically interacts with Ret receptor
CC protein, triggering Ret dimerisation and/or autophosphorylation of the
CC Ret tyrosine kinase domain. Vectors containing retL3 DNA and prokaryotic
CC or eukaryotic host cells transformed or transfected with these vectors
CC are claimed, as well as a method for production of RetL3, its soluble
CC variants and fusion proteins with a toxin, imageable compound or
CC radionuclide. RetL3, optionally when expressed from vectors in vivo, is
CC used to promote growth of new tissue and survival of damaged tissue,
CC particularly kidney or neural tissue. Typical applications are in renal
CC failure, nephritis, kidney transplants, toxic or hypoxic injury,
CC neurodegeneration, motor neurone disease, multiple sclerosis, bacterial,
CC viral or prion infections (e.g. meningitis, myelopathy associated with
CC HIV or Creutzfeldt-Jakob disease), cranial nerve or spinal cord injury,
CC developmental disorders such as Down's syndrome and cerebral palsy, or
CC conditions involving the peripheral nervous system (Lyme disease,
CC muscular dystrophy and myasthenia gravis). Fusion proteins are used to
CC deliver toxins etc. to Ret-expressing cells, especially tumours

XX SQ Sequence 397 AA;

Query Match 100.0%; Score 2131; DB 2; Length 397;
Best Local Similarity 100.0%; Pred. No. 3.5e-198;
Matches 397; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGLSWSPRPPLMLLVLSLMLPLGAGNSLATENRFVNSCTQARKKCEANPACKAAYOH 60
DB 1 MGLSWSPRPPLMLLVLSLMLPLGAGNSLATENRFVNSCTQARKKCEANPACKAAYOH 60
QY 61 LGSCTSSLSRPLPLEESAMSDCLEAAEQLRNSSLIDCRCHRRMKHQATCLDIYTWVHPA 120
DB 61 LGSCTSSLSRPLPLEESAMSDCLEAAEQLRNSSLIDCRCHRRMKHQATCLDIYTWVHPA 120
QY 121 RSLGDYELDVSPYEDVTTSKPKWKNLSKLNMLKPDSDCLCKFAMLCTLHDKCDRLRKAYG 180
DB 121 RSLGDYELDVSPYEDVTTSKPKWKNLSKLNMLKPDSDCLCKFAMLCTLHDKCDRLRKAYG 180
QY 181 EACSGIRCOHCLCLAQRSFFKAAESHAQGLLCCPCAPEDAGGERRRNTIAPSCALPS 240
DB 181 EACSGIRCOHCLCLAQRSFFKAAESHAQGLLCCPCAPEDAGGERRRNTIAPSCALPS 240
QY 241 VTPNCLDLRFCDPLCRSLMDFOFTHCPMDILGTGTEQSRCLRAYLGLGTAMTPN 300
DB 241 VTPNCLDLRFCDPLCRSLMDFOFTHCPMDILGTGTEQSRCLRAYLGLGTAMTPN 300
QY 301 FISKVNTVALSCTCRSGNLDQCEQLERSFSONPCLVEIAIAKORFHRQLFSQDWADS 360
DB 301 FISKVNTVALSCTCRSGNLDQCEQLERSFSONPCLVEIAIAKORFHRQLFSQDWADS 360
QY 361 TFSVVOQNSNPALRLOPRILPSFSLPILLLQTLW 397
DB 361 TFSVVOQNSNPALRLOPRILPSFSLPILLLQTLW 397

RESULT 2

AA84591

ID AA84591 standard; protein; 397 AA.

XX AC AA84591;

XX DT 25-JUL-2000 (first entry)

XX DE Amino acid sequence of a human growth factor receptor-alpha precursor.

XX Human; artemin; growth factor; neurotrophic factor; trophic support;
KW neuron; trigeminal ganglion neuron; nodose ganglion neuron;
KW superior cervical ganglion neuron; midbrain neuron; Alzheimer's disease;
KW peripheral neuropathy; amyotrophic lateral sclerosis; ischemic stroke;
KW Parkinson's disease; Huntington's disease; acute brain injury;
KW acute spinal cord injury; nervous system tumour; blastoma;
KW multiple sclerosis; infection; enteric disease; idiopathic constipation;
KW Parkinson's disease; small cell lung carcinoma.

OS Mus sp.
XX Key Location/Qualifiers
FH Peptide 1..28 /note= "signal peptide"
FT Protein 29..369 /note= "mature protein"
FT Modified-site 92
FT Modified-site 145 /note= "putative N-linked glycosylation site"
FT Modified-site 145 /note= "putative N-linked glycosylation site"
FT Modified-site 306 /note= "putative N-linked glycosylation site"
XX WO200018799-A1.

XX 06-APR-2000.

XX 29-SEP-1999; 99WO-US022604.

XX 29-SEP-1998; 98US-00163283.

XX 12-NOV-1998; 98US-0108148P.

XX 22-DEC-1998; 98US-00218698.

XX (UNIW) UNIV WASHINGTON.

XX Milbrandt JD, Baloh RH;

XX WPI; 2000-293109/25.

XX Isolated artemin growth factor proteins and the nucleic acids that encode
PT them, useful for treating a range of degenerative neuronal disorders such
PT as Parkinson's disease and Huntington's disease.

XX Disclosure; Fig 12; 96pp; English.

XX The present sequence represents a murine growth factor receptor-alpha
CC precursor. The specification describes an artemin growth factor protein.
CC Artemin is a neurotrophic factor that belongs to the GDNF (glial cell
CC line-derived neurotrophic factor)/neurturin/persephin family of growth
CC factors and promotes differentiation, maintains mature phenotype and
CC provides trophic support, promoting growth and survival of neurons.
CC Artemin promotes the survival of trigeminal ganglion neurons and tyrosine-
CC hydroxylase-expressing dopaminergic ventral midbrain neurons. Artemin is
CC the only member of the GDNF family that binds to GFR-alpha (growth factor
CC receptor-alpha) and activates the GFR-alpha3/RET (Ret protein-tyrosine
CC kinase) receptor complex and additionally, like GDNF and neurturin,
CC artemin also binds to and activates GFRalpha1/RET. Artemin polypeptides
CC and polynucleotides are administered to treat peripheral neuropathy,
CC amyotrophic lateral sclerosis, Alzheimer's disease, Parkinson's disease,
CC Huntington's disease, ischemic stroke, acute brain injury, acute spinal
CC cord injury, a nervous system tumour (e.g. blastomas) multiple
CC sclerosis, infection or enteric disease (e.g. idiopathic constipation or
CC constipation associated with Parkinson's disease, spinal cord injury or
CC use of opiate pain killers). They may also be used to treat a patient
CC suffering from small cell lung carcinoma

XX SQ Sequence 397 AA;

Query Match 100.0%; Score 2131; DB 3; Length 397;
Best Local Similarity 100.0%; Pred. No. 3.5e-198;
Matches 397; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGLSWSPRPPLMLLVLSLMLPLGAGNSLATENRFVNSCTQARKKCEANPACKAAYOH 60
DB 1 MGLSWSPRPPLMLLVLSLMLPLGAGNSLATENRFVNSCTQARKKCEANPACKAAYOH 60
QY 61 LGSCTSSLSRPLPLEESAMSDCLEAAEQLRNSSLIDCRCHRRMKHQATCLDIYTWVHPA 120
DB 61 LGSCTSSLSRPLPLEESAMSDCLEAAEQLRNSSLIDCRCHRRMKHQATCLDIYTWVHPA 120
QY 121 RSLGDYELDVSPYEDVTTSKPKWKNLSKLNMLKPDSDCLCKFAMLCTLHDKCDRLRKAYG 180

Db 121 RSLGDIYELVSPYEDVTTSKPKMNLKLNMLKPDSDCLCKFAMLCITLHDKCDRLKAYG 180
 QY 181 EACSGIRCORHLCLAQLRSEFFKAAESHAQGLLLCPAPEDAGCGERRNTIAPSCALPS 240
 Db 181 EACSGIRCORHLCLAQLRSEFFKAAESHAQGLLLCPAPEDAGCGERRNTIAPSCALPS 240
 QY 241 VTPNCLDLRSFCRADPLCRSLMDFOFTHCHPMDILGTCAEQSRCLRAYLGLIGTAMTPN 300
 Db 241 VTPNCLDLRSFCRADPLCRSLMDFOFTHCHPMDILGTCAEQSRCLRAYLGLIGTAMTPN 300
 QY 301 FISKVNTTVALSCTCRSGNLODECEQLERSFSQNPCLVEAIAAKMRFHRLFSQDWADS 360
 Db 301 FISKVNTTVALSCTCRSGNLODECEQLERSFSQNPCLVEAIAAKMRFHRLFSQDWADS 360
 QY 361 TFSVVOQNSNPALRLOPRLPILSILPILLOTLM 397
 Db 361 TFSVVOQNSNPALRLOPRLPILSILPILLOTLM 397

RESULT 3
 ID AAY15174
 AC AAY15174 standard; protein; 397 AA.
 XX AAY15174;
 DT 07-FEB-2000 (first entry)
 XX Murine GFRalpha3.
 DE Murine GFRalpha3;
 KW Glial-cell-line-derived neurotrophic factor family receptor alpha-3;
 KW probe; homologous DNA; neuronal cell activation; GFRalpha3 ligand;
 KW cell proliferation; cell differentiation; GFRalpha3-containing cell;
 KW Ret-containing cell; peripheral nervous system disease; diabetes;
 KW human immunodeficiency virus; chemotherapeutic agent treatment;
 KW autonomic nervous system dysfunction; transgenic animal.
 XX Mus musculus.
 FH Key
 FT Peptide
 FT 1..27 Location/Qualifiers
 FT /label= signal_peptide
 FT Modified-site 92..95
 FT /note= "Potential glycosylation site"
 FT Modified-site 145..148
 FT /note= "Potential glycosylation site"
 FT Region 392..397
 FT /note= "C-terminal hydrophobic sequence associated with GPI-anchoring"
 XX WO9949039-A2.
 XX 30-SEP-1999.
 XX 19-MAR-1999; 99WO-US006098.
 XX 23-MAR-1998; 98US-0079124P.
 XX 13-APR-1998; 98US-0081569P.
 XX (GETH) GENENTECH INC.
 XX De Sauvage FJ, Klein RD, Phillips HS, Rosenthal A;
 XX WPI; 2000-038358/03.
 XX N-PSDB; AAZ29100.
 XX New isolated GFR-alpha3 nucleic acid, used to develop products for
 XX treating diseases or conditions involving peripheral nervous system or
 XX autonomic nervous system.
 XX Example 1; Fig 1; 112pp; English.
 XX

CC The present sequence is the full length mouse glial-cell-line-derived
 CC neurotrophic factor family receptor alpha-3 (GFRalpha3). This has
 CC sequence identity with GFRalpha1. GFRalpha3 DNA or its fragments can be
 CC used as a probe to screen for homologous DNA. GFRalpha3 possesses neuronal
 CC cell activation property. GFRalpha3 ligands can be used to stimulate
 CC proliferation, growth, survival, differentiation, metabolism or
 CC regeneration of GFRalpha3- and Ret-containing cells. They can be useful
 CC in the treatment of peripheral nervous system diseases, eg. those
 CC associated with diabetes, human immunodeficiency virus, or
 CC chemotherapeutic agent treatments. Agonist or antagonists of GFRalpha3
 CC can be used to treat autonomic nervous system dysfunctions. The products
 CC can also be used for detection, diagnosis and production of transgenic
 CC animals
 XX Sequence 397 AA;
 SQ

Query Match 100.0%; Score 2131; DB 3; Length 397;
 Best Local Similarity 100.0%; Pred. No. 3.5e-198;
 Matches 397; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGLSNSPRPPLMLILLVLSLMLPLGAGNSLATENFVNSCTQARKKCEANPACKAAYQH 60
 Db 1 MGLSNSPRPPLMLILLVLSLMLPLGAGNSLATENFVNSCTQARKKCEANPACKAAYQH 60
 QY 61 LGSCTSSLSRPLPLEESAMSDCLEAAEQLRNSSLIDCRHRMKHQATCLDIYTVHPA 120
 Db 61 LGSCTSSLSRPLPLEESAMSDCLEAAEQLRNSSLIDCRHRMKHQATCLDIYTVHPA 120
 QY 121 RSLGDIYELVSPYEDVTTSKPKMNLKLNMLKPDSDCLCKFAMLCITLHDKCDRLKAYG 180
 Db 121 RSLGDIYELVSPYEDVTTSKPKMNLKLNMLKPDSDCLCKFAMLCITLHDKCDRLKAYG 180
 QY 181 EACSGIRCORHLCLAQLRSEFFKAAESHAQGLLLCPAPEDAGCGERRNTIAPSCALPS 240
 Db 181 EACSGIRCORHLCLAQLRSEFFKAAESHAQGLLLCPAPEDAGCGERRNTIAPSCALPS 240
 QY 241 VTPNCLDLRSFCRADPLCRSLMDFOFTHCHPMDILGTCAEQSRCLRAYLGLIGTAMTPN 300
 Db 241 VTPNCLDLRSFCRADPLCRSLMDFOFTHCHPMDILGTCAEQSRCLRAYLGLIGTAMTPN 300
 QY 301 FISKVNTTVALSCTCRSGNLODECEQLERSFSQNPCLVEAIAAKMRFHRLFSQDWADS 360
 Db 301 FISKVNTTVALSCTCRSGNLODECEQLERSFSQNPCLVEAIAAKMRFHRLFSQDWADS 360
 QY 361 TFSVVOQNSNPALRLOPRLPILSILPILLOTLM 397
 Db 361 TFSVVOQNSNPALRLOPRLPILSILPILLOTLM 397

RESULT 4
 ADJ58709
 ID ADJ58709 standard; protein; 397 AA.
 XX ADJ58709;
 XX 06-MAY-2004 (first entry)
 XX Murine retL3 protein.
 XX Tissue growth; retL protein; organ failure; foetal malformation;
 XX tumour growth; renal tissue; cytostatic; vulnerary; nephrotropic; murine.
 XX Mus sp.
 XX US6677135-B1.
 XX 13-JAN-2004.
 XX 06-NOV-1998; 98US-00187906.
 XX 08-MAY-1996; 96US-0017427P.
 XX 07-JUN-1996; 96US-0019300P.
 XX 16-JUL-1996; 96US-0021859P.

PR 23-AUG-1996; 96US-0023444P.
 PR 11-APR-1997; 97US-0043533P.
 PR 07-MAY-1997; 97WO-US007726.
 XX
 PA (BIOJ) BIOGEN INC.
 XX
 PI Sanicola-Nadel M, Hession C, Cate RL, Worley DS;
 XX
 XX WPI; 2004-079845/08.
 DR N-PSDB; ADY58708.
 XX
 XX New nucleic acid encoding Ret polypeptide, useful for diagnosing and/or
 PT treating diseases or conditions associated with aberrant expression or
 PT activity of the Ret ligand, such as organ failure, fetal malformations
 PT and tumor growth.
 XX
 XX Claim 1; SEQ ID NO 17; 66pp; English.
 XX
 CC The present invention relates to nucleotide and amino acid sequences
 CC which promote tissue growth and methods for modulating tissue growth. The
 CC invention also relates to retL proteins and polynucleotides encoding such
 CC proteins. RetL proteins interact with a receptor protein Ret to trigger
 CC dimerisation and/or autophosphorylation of the tyrosine kinase domain of
 CC the receptor protein Ret. The methods and compositions of the present
 CC invention are useful for the diagnosis and/or treatment of diseases or
 CC conditions associated with aberrant expression or activity of the Ret
 CC ligand, such as organ failure, foetal malformations and tumour growth and
 CC for promoting regeneration or survival of damaged renal tissue. The
 CC present sequence is murine retL3 protein of the invention.
 XX
 SQ Sequence 397 AA;

Query Match 100.0%; Score 2131; DB 8; Length 397;
 Best Local Similarity 100.0%; Pred. No. 3.5e-198;
 Matches 397; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGLSWSPRPPLMLLLVLSLWPLGAGNSLATENRFVNSCTQARKKCEANPACKAAYOH 60
 DB 1 MGLSWSPRPPLMLLLVLSLWPLGAGNSLATENRFVNSCTQARKKCEANPACKAAYOH 60
 QY 61 LGSCTSSLSRPLPLEESAMSADCLEAAEQRLNSLIDCRCHRMKHQATCLDIYTVHPA 120
 DB 61 LGSCTSSLSRPLPLEESAMSADCLEAAEQRLNSLIDCRCHRMKHQATCLDIYTVHPA 120
 QY 121 RSLGDIYELDVSPYEDVTTSKPWQWNLKLNMLKPDSDCLCFAMLCITLHDKCDRLKAYG 180
 DB 121 RSLGDIYELDVSPYEDVTTSKPWQWNLKLNMLKPDSDCLCFAMLCITLHDKCDRLKAYG 180
 QY 181 EACSGIRCORHLCIAQLRSFFFEKAAESHAQGLLLCPAPEDAGCGERRNTIAPSCALPS 240
 DB 181 EACSGIRCORHLCIAQLRSFFFEKAAESHAQGLLLCPAPEDAGCGERRNTIAPSCALPS 240
 QY 241 VTPNCILDRSFCRADPLCRSLRMDFTQTHCPMDILGTCAEQSRCLRAYLGLIGTAMTNP 300
 DB 241 VTPNCILDRSFCRADPLCRSLRMDFTQTHCPMDILGTCAEQSRCLRAYLGLIGTAMTNP 300
 QY 301 FISKVNTVALSCTCRGSGNLQDECEQLERSFSQNPCLVEAIAAKVRFHQPLFSQDWADS 360
 DB 301 FISKVNTVALSCTCRGSGNLQDECEQLERSFSQNPCLVEAIAAKVRFHQPLFSQDWADS 360
 QY 361 TFSVVOQNSNPALRQLPRLPILSILPILLOTILW 397
 DB 361 TFSVVOQNSNPALRQLPRLPILSILPILLOTILW 397

RESULT 5
 ADY53845
 ID ADY53845 standard; protein; 397 AA.
 XX
 XX ADY53845;
 XX
 DT 05-MAY-2005 (first entry)
 XX

DE Mouse retL3 protein.
 XX
 KW DNA purification; immune stimulation; ret ligand.
 XX
 OS Mus sp.
 XX
 PN US6861509-B1.
 XX
 PD 01-MAR-2005.
 XX
 PF 21-JAN-2000; 2000US-00489407.
 XX
 PR 08-MAY-1996; 96US-0017427P.
 PR 07-JUN-1996; 96US-0019300P.
 PR 16-JUL-1996; 96US-0021859P.
 PR 23-AUG-1996; 96US-0023444P.
 PR 11-APR-1997; 97US-0043533P.
 PR 07-MAY-1997; 97WO-US007726.
 PR 06-NOV-1998; 98US-00187906.
 XX
 XX (BIOJ) BIOGEN INC.
 PA
 XX Sanicola-Nadel M, Hession C, Cate RL, Worley DS;
 PI
 XX WPI; 2005-201184/21.
 DR N-PSDB; ADY53844.
 XX
 XX New anti-Ret ligand (RetL) antibody, useful for treating acute renal
 PT failure, acute nephritis, chronic renal failure, nephritic syndrome, as
 PT well as Alzheimer's disease, Parkinson's and multiple sclerosis.
 XX
 PS Disclosure; SEQ ID NO 17; 66pp; English.
 XX
 XX The invention relates to an antibody produced by a hybridoma selected
 CC from the group consisting of AA.FF9 and AA.GE7.3. The antibody is used to
 CC stimulate neural and renal cell growth. This sequence corresponds to a
 CC protein sequence of the invention.
 XX
 SQ Sequence 397 AA;

Query Match 100.0%; Score 2131; DB 9; Length 397;
 Best Local Similarity 100.0%; Pred. No. 3.5e-198;
 Matches 397; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGLSWSPRPPLMLLLVLSLWPLGAGNSLATENRFVNSCTQARKKCEANPACKAAYOH 60
 DB 1 MGLSWSPRPPLMLLLVLSLWPLGAGNSLATENRFVNSCTQARKKCEANPACKAAYOH 60
 QY 61 LGSCTSSLSRPLPLEESAMSADCLEAAEQRLNSLIDCRCHRMKHQATCLDIYTVHPA 120
 DB 61 LGSCTSSLSRPLPLEESAMSADCLEAAEQRLNSLIDCRCHRMKHQATCLDIYTVHPA 120
 QY 121 RSLGDIYELDVSPYEDVTTSKPWQWNLKLNMLKPDSDCLCFAMLCITLHDKCDRLKAYG 180
 DB 121 RSLGDIYELDVSPYEDVTTSKPWQWNLKLNMLKPDSDCLCFAMLCITLHDKCDRLKAYG 180
 QY 181 EACSGIRCORHLCIAQLRSFFFEKAAESHAQGLLLCPAPEDAGCGERRNTIAPSCALPS 240
 DB 181 EACSGIRCORHLCIAQLRSFFFEKAAESHAQGLLLCPAPEDAGCGERRNTIAPSCALPS 240
 QY 241 VTPNCILDRSFCRADPLCRSLRMDFTQTHCPMDILGTCAEQSRCLRAYLGLIGTAMTNP 300
 DB 241 VTPNCILDRSFCRADPLCRSLRMDFTQTHCPMDILGTCAEQSRCLRAYLGLIGTAMTNP 300
 QY 301 FISKVNTVALSCTCRGSGNLQDECEQLERSFSQNPCLVEAIAAKVRFHQPLFSQDWADS 360
 DB 301 FISKVNTVALSCTCRGSGNLQDECEQLERSFSQNPCLVEAIAAKVRFHQPLFSQDWADS 360
 QY 361 TFSVVOQNSNPALRQLPRLPILSILPILLOTILW 397
 DB 361 TFSVVOQNSNPALRQLPRLPILSILPILLOTILW 397

RESULT 6
ADZ00209
ID ADZ00209 standard; protein; 397 AA.
XX
AC ADZ00209;
XX
DT 30-JUN-2005 (first entry)
XX
DE Mouse Ret ligand 3 (RetL3), SEQ ID NO:17.
XX
KW Cell growth; development; signal transduction; neurological disease;
KW renal disease; genitourinary disease; neuroprotective; nephrotropic;
KW cancer; neoplasm; cytostatic; RetL3;
KW Ret tyrosine kinase receptor ligand 3; Ret ligand 3;
KW GDNF family receptor alpha 3; GFRA3.
XX
OS Mus sp.
XX
PN US2005080235-A1.
XX
PD 14-APR-2005.
XX
PP 23-SEP-2003; 2003US-00668936.
XX
PR 08-MAY-1996; 96US-0017427P.
PR 07-JUN-1996; 96US-0019300P.
PR 16-JUL-1996; 96US-0021859P.
PR 23-AUG-1996; 96US-0023444P.
PR 11-APR-1997; 97US-0043533P.
PR 07-MAY-1997; 97WO-US0007726.
PR 06-NOV-1998; 98US-00187906.
XX
(SANI/) SANICOLA-NADEL M.
PA (HESS/) HESSION C.
PA (CATE/) CATE R L.
PA (WORL/) WORLEY D S.
XX
PI Sanicola-Nadel M, Hession C, Cate RL, Worley DS;
XX
DR WPI; 2005-305025/31.
DR N-PSDB; ADZ00208.
XX
PT New polypeptide sequence that interacts with a receptor protein Ret to
PT trigger dimerization or autophosphorylation, useful in preparing a
PT composition for treating neurodegenerative disorders, e.g., Alzheimer's
PT disease.
XX
PS Claim 1; SEQ ID NO 17; 67pp; English.
XX
CC The invention relates to the murine and human RetL3 (Ret ligand 3)
CC proteins (ADZ00209 and ADZ00213, respectively) and to proteins at least
CC 80% identical to murine or human RetL3. The invention also discloses
CC other RetL proteins such as rat RetL1, human RetL1, human RetL2,
CC fragments of human RetL1, mouse RetL3 and human RetL3, and cDNA sequences
CC encoding these RetL proteins or protein fragments. Like other RetL
CC proteins, the RetL3 proteins of the invention interact with the Ret
CC receptor tyrosine kinase that is encoded by the Ret proto-oncogene,
CC triggering Ret receptor dimerization or autophosphorylation. The Ret
CC receptor is expressed during development in a variety of tissues,
CC including the peripheral and central nervous systems and the kidney. It
CC is also expressed in some cancers. RetL proteins such as the murine and
CC human RetL3 proteins, and RetL polynucleotides may be used for
CC stimulating Ret receptor signaling, thereby promoting renal or neuronal
CC cell growth or survival and minimizing damage to such tissues after
CC various insults. They may therefore be used to treat renal disorders
CC (e.g., renal failure, renal tube defects and renal trauma) or
CC neurological disorders including neurodegenerative disorders (e.g.,
CC Alzheimer's disease), bacterial or viral diseases of the nervous system
CC (e.g., meningitis), neurological damage (e.g. that caused by hemorrhage
CC or trauma) and developmental neural disorders (e.g., mental retardation).
CC Conversely, antibodies against RetL may be used to block RetL-Ret
CC receptor signal transduction for inhibiting tumor growth, fusion proteins
CC comprising a RetL protein are useful for targeting a drug to Ret receptor

CC -expressing tumors. Anti-RetL antibodies and RetL fusion proteins may
CC also be used in medical imaging. The present sequence represents a
CC specifically claimed full-length murine RetL3 protein encoded by cDNA
CC isolated in the invention.
XX
SQ Sequence 397 AA;
Query Match 100.0%; Score 2131; DB 9; Length 397;
Best Local Similarity 100.0%; Pred. No. 3.5e-198;
Matches 397; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGLSWSPRPPLMLILLVLSLWPLGAGNSLATENRFVNSCTOARKKCEANPACKAAYQH 60
DB 1 MGLSWSPRPPLMLILLVLSLWPLGAGNSLATENRFVNSCTOARKKCEANPACKAAYQH 60
QY 61 LGSCTSSLRPLPLEESAMSDCLEAEQLRNSLIDCRHRRMKHOATCLDIYVTVHPA 120
DB 61 LGSCTSSLRPLPLEESAMSDCLEAEQLRNSLIDCRHRRMKHOATCLDIYVTVHPA 120
QY 121 RSLGDYELDVSPYEDVTTSKPMKONLSKLNMLKPDSDCLCKFAMLCCTLHDKCDRLRKAYG 180
DB 121 RSLGDYELDVSPYEDVTTSKPMKONLSKLNMLKPDSDCLCKFAMLCCTLHDKCDRLRKAYG 180
QY 181 EACSGIRCQRHLCIAQLRSFFFEKAAESHAQGLLLCPACEDACGRRRTNTIAPSCALPS 240
DB 181 EACSGIRCQRHLCIAQLRSFFFEKAAESHAQGLLLCPACEDACGRRRTNTIAPSCALPS 240
QY 241 VTPNCUDLRSFCRADPLCRSLRMDFTCHPMDILGTCATEQSRCLRAYLGLGTAMTPN 300
DB 241 VTPNCUDLRSFCRADPLCRSLRMDFTCHPMDILGTCATEQSRCLRAYLGLGTAMTPN 300
QY 301 FISKVNTTVALSCTCRGSGNLQDECEQLERSFSQNPCLVEAIAAKRFRHQLFSQDWADS 360
DB 301 FISKVNTTVALSCTCRGSGNLQDECEQLERSFSQNPCLVEAIAAKRFRHQLFSQDWADS 360
QY 361 TFSVVOQNSNPALRLOPRLPILSPILPILLOTLM 397
DB 361 TFSVVOQNSNPALRLOPRLPILSPILPILLOTLM 397
RESULT 7
AAW84182
ID AAW84182 standard; protein; 397 AA.
XX
AC AAW84182;
XX
DT 25-MAR-1999 (first entry)
XX
DE A GDNFR-alpha-related protein 3 (GRR3).
XX
KW Rat; glial cell-line derived neurotrophic factor receptor; GDNFR;
KW glial cell line-derived neurotrophic factor; GDNF; neurturin;
KW signal transduction; dopaminergic nerve cell; Parkinson's disease;
KW Alzheimer's disease; amyotrophic lateral sclerosis;
KW neurological disorder; diabetes; glaucoma; sensory neuron;
KW retinal ganglion cell degeneration; sensory neuropathy; retinopathy;
KW gene therapy; GDNFR-related protein 3; GRR3.
XX
OS Rattus sp.
XX
PN WO9854213-A2.
XX
PP 03-DEC-1998.
XX
PR 27-APR-1998; 98WO-US008486.
XX
PR 30-MAY-1997; 97US-00866354.
XX
PA (AMGE-) AMGEN INC.
XX
PI Fox GM, Jing S, Wen D;
XX
DR WPI; 1999-080806/07.

DR N-PSDB; AAV99331.
 XX New isolated glial cell line-derived neurotrophic factor receptors - used
 PT to develop products for treating e.g. improperly functioning dopaminergic
 FT nerve cells, Parkinson's disease, Alzheimer's disease or amyotrophic
 PT lateral sclerosis.
 XX
 XX Claim 51; Fig 17; 310pp; English.
 XX
 CC The present sequence represents a rat glial cell-line derived
 CC neurotrophic factor receptor (GDNFR)-related protein 3 (GRR3). The
 CC protein has similar functions to GDNFR. GDNFR proteins are functionally
 CC characterised by the ability to bind glial cell line-derived neurotrophic
 CC factor (GDNF) and/or neurturin specifically, and to act as part of a
 CC molecular complex which mediates or enhances the signal transduction
 CC affects of GDNF and/or neurturin. The proteins can be used for treating
 CC Alzheimer's disease or amyotrophic lateral sclerosis. They can also be
 CC used for treating neurological disorders associated with diabetes,
 CC glaucoma or other diseases and conditions involving retinal ganglion cell
 CC degeneration, sensory neuropathy caused by injury to, insults to, or
 CC degeneration of, sensory neurons, pathological conditions, or disease or
 CC injury-related retinopathies. The products can also be used for
 CC detection, diagnosis, drug screening and gene therapy
 XX
 XX Sequence 397 AA;

Query Match 92.5%; Score 1972; DB 2; Length 397;
 Best Local Similarity 92.9%; Pred. No. 1e-182;
 Matches 369; Conservative 9; Mismatches 19; Indels 0; Gaps 0;
 QY 1 MGLSWSPRLMILLVLSMLPLGAGNSLATENRFVNSCTQARKKCEANPACAAAYOH 60
 DB 1 MGLSRSPRPPLVILLVLSMLPLGTGNSLPTENLRFVNSCTQARKKCEANPACAAAYOH 60
 QY 61 LGSCTSSLRPLPLEESAMSADCLEAAEQLRNSSLIDCRHRMKHQATCLDIYTVHPA 120
 DB 61 LDSCTPSLSPLPSGESATSAACLEAAQQLRNSLIDCRHRMKHQATCLDIYTVHPV 120
 QY 121 RSLGVDYELVSPYEDVTTSKPMKQNLKSLNMLKPDSDCLCKFAMLCITLHDKDRLKAYG 180
 DB 121 RSLGVDYELVSPYEDVTTSKPMKQNLKSLNMLKPDSDCLCKFAMLCITLHDKDRLKAYG 180
 QY 181 EACSGIRCORHLCLAOIRSFPEKAESHAQGLLLCPAPEDAGCGRRNTTAPSCALPS 240
 DB 181 EACSGIRCORHLCLAOIRSFPEKAESHAQGLLLCPAPEDAGCGRRNTTAPSCALPS 240
 QY 241 VTPNCLDLRSFCRADPLCRSLMDFTQTHCHPMDILGTCAEQSRCLRAYLIGLIGTAMTNP 300
 DB 241 VAPNCLDLRSFCRADPLCRSLMDFTQTHCHPMDILGTCAEQSRCLRAYLIGLIGTAMTNP 300
 QY 301 FISKVNTVALSCTCRSGNLODECEQLERSFSQNPCLVEATAAKMRFHQLFPSQWADS 360
 DB 301 FISKVNTVALGCTCRSGNLODECEQLERSFSQNPCLMEATAAKMRFHQLFPSQWADS 360
 QY 361 TFSVMOQNSPALRQPLRPILSILPLILLQTLW 397
 DB 361 TFSVMOQNSPALRQPLRPILSILPLILLQTLW 397

RESULT 8
 AAY15182
 ID AAY15182 standard; protein; 888 AA.
 XX
 XX AAY15182;
 XX
 DT 07-FEB-2000 (first entry)
 XX
 DE gd-GFRalpha3-Rse-gd chimeric receptor.
 XX
 KW gd-GFRalpha3-Rse-gd chimeric receptor; gd epitope tag; murine GFRalpha3;
 KW GPI signal; human GFRalpha3; Rse tyrosine kinase receptor; pSV1 vector;
 KW recombinant PCR; SV40 promoter; agonist antibody; natural ligand.

XX Synthetic.
 OS
 XX Key Location/Qualifiers
 FH 110..386
 FT Region
 FT /note= "Ligand binding region"
 XX
 XX WO9949039-A2.
 XX
 XX 30-SEP-1999.
 PD
 XX 19-MAR-1999; 99WO-US006098.
 PF
 XX 23-MAR-1998; 98US-0079124P.
 PR
 XX 13-APR-1998; 98US-0081569P.
 PR
 XX (GETH) GENENTECH INC.
 PA
 XX De Sauvage FJ, Klein RD, Phillips HS, Rosenthal A;
 PI WPI; 2000-038358/03.
 XX
 XX New isolated GFR-alpha3 nucleic acid, used to develop products for
 XX treating diseases or conditions involving peripheral nervous system or
 XX autonomic nervous system.
 PT
 XX
 XX Claim 9; Page 107-110; 112pp; English.
 PS
 XX The present sequence is gd-GFRalpha3-Rse-gd chimeric receptor. This was
 CC constructed with the gd epitope tag followed by the murine GFRalpha3
 CC extracellular domain (less the GPI signal; preferably the human
 CC GFRalpha3) followed by the transmembrane and intracellular domain of the
 CC Rse tyrosine kinase receptor and another gp epitope tag. This construct
 CC was assembled by recombinant PCR into a pSV1 vector under the control of
 CC the SV40 promoter. This is used in an assay to identify agonist
 CC antibodies and a natural ligand for mammalian GFRalpha3
 XX
 XX Sequence 888 AA;
 SQ
 Query Match 88.2%; Score 1880; DB 3; Length 888;
 Best Local Similarity 94.1%; Pred. No. 2.8e-173;
 Matches 354; Conservative 5; Mismatches 11; Indels 6; Gaps 1;
 QY 25 LAGNSLATENRFVNSCTQARKKCEANPACAAAYOHLSGCTSSLSRPLPLEESAMSADCL 84
 DB 54 LEAGNSLATENRFVNSCTQARKKCEANPACAAAYOHLSGCTSSLSRPLPLEESAMSADCL 113
 QY 85 EAAEQLRNSSLIDCRHRMKHQATCLDIYTVHPARSLGVDYELVSPYEDVTTSKPMK 144
 DB 114 EAAEQLRNSSLIDCRHRMKHQATCLDIYTVHPARSLGVDYELVSPYEDVTTSKPMK 173
 QY 145 NLSKLNMLKPDSDCLCKFAMLCITLHDKDRLKAYGACSGIRCORHLCLAOIRSFPEKA 204
 DB 174 NLSKLNMLKPDSDCLCKFAMLCITLHDKDRLKAYGACSGIRCORHLCLAOIRSFPEKA 233
 QY 205 AESHAQGLLLCPAPEDAGCGRRNTTAPSCALPSVTPNCLDLRSFCRADPLCRSLMD 264
 DB 234 AESHAQGLLLCPAPEDAGCGRRNTTAPSCALPSVTPNCLDLRSFCRADPLCRSLMD 293
 QY 265 FQTHCHPMDILGTCAEQSRCLRAYLIGLIGTAMTNPFIKVNNTVALSCTCRSGNLODE 324
 DB 294 FQTHCHPMDILGTCAEQSRCLRAYLIGLIGTAMTNPFIKVNNTVALSCTCRSGNLODE 353
 QY 325 CEQLERSFSQNPCLVEATAAKMRFHQLFPSQWADSTFSVMOQNSPALR-----LQP 378
 DB 354 CEQLERSFSQNPCLVEATAAKMRFHQLFPSQWADSTFSVMOQNSPALR-----LQP 413
 QY 379 RLPILSILPLILLQ 394
 DB 414 LTAALVTAALAILLR 429
 RESULT 9

QY 128 LDVSPYEDVTTSKPKWKNLSKLNMLKPDSDLCCLKFAMLCITLHDKCDRLKAYGEACSGIR 187
 DB 77 LDVSPYEDVTTSKPKWKNLSKLNMLKPDSDLCCLKFAMLCITLHDKCDRLKAYGEACSGIR 136
 QY 188 CORHLCLAQLRSPFFKAEASHAQLLPCAPEDAGCGERRNTIAPSCALPSVTPNCLD 247
 DB 137 CORHLCLAQLRSPFFKAEASHAQLLPCAPEDAGCGERRNTIAPSCALPSVTPNCLD 196
 QY 248 LRSFCRADPLCRSRLMDFQTHCHPMDILGTCAEQSRCLRAYLGLIGTAMTNPFSKVT 307
 DB 197 LRSFCRADPLCRSRLMDFQTHCHPMDILGTCAEQSRCLRAYLGLIGTAMTNPFSKVT 256
 QY 308 TVALSCTCRSGNLODECEQLERSFSQNPCLVEAIAAKWRFHQLFQSDWADSTFSVVOQ 367
 DB 257 TVALSCTCRSGNLODECEQLERSFSQNPCLVEAIAAKWRFHQLFQSDWADSTFSVVOQ 316
 QY 368 QNSNPALRLQPRLPILSILPLILLQTLW 397
 DB 317 QNSNPALRLQPRLPILSILPLILLQTLW 346
 RESULT 11
 ADY53843
 ID ADY53843 standard; protein; 346 AA.
 XX ADY53843;
 XX
 DT 05-MAY-2005 (first entry)
 XX
 DE Partial mouse retL3 protein.
 XX
 KW DNA purification; immune stimulation; ret ligand.
 XX
 OS Mus sp.
 XX
 PN US681509-B1.
 XX
 PD 01-MAR-2005.
 XX
 PF 21-JAN-2000; 2000US-00489407.
 XX
 PR 08-MAY-1996; 96US-0017427P.
 PR 07-JUN-1996; 96US-0019300P.
 PR 16-JUL-1996; 96US-0021859P.
 PR 23-AUG-1996; 96US-0023444P.
 PR 11-APR-1997; 97US-0043533P.
 PR 07-MAY-1997; 97WO-US007726.
 PR 06-NOV-1998; 98US-00187906.
 XX
 PA (BIOJ) BIOGEN INC.
 XX
 PI Sanicola-Nadel M, Hession C, Cate RL, Worley DS;
 XX
 XX WPI; 2005-201184/21.
 DR N-PSDB; ADY53842.
 XX
 PT New anti-Ret ligand (RetL) antibody, useful for treating acute renal failure, acute nephritis, chronic renal failure, nephritic syndrome, as well as Alzheimer's disease, Parkinson's and multiple sclerosis.
 FT
 XX Disclosure; SEQ ID NO 15; 66pp; English.
 PS
 CC The invention relates to an antibody produced by a hybridoma selected from the group consisting of AA.FF9 and AA.G87.3. The antibody is used to stimulate neural and renal cell growth. This sequence corresponds to a protein sequence of the invention.
 CC
 XX Sequence 346 AA;
 SQ
 Query Match 83.2%; Score 1774; DB 9; Length 346;
 Best Local Similarity 100.0%; Pred. No. 1.6e-163;
 Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 68 LSRPLPLEESAMSDCLEAAEQLRNSSLIDCRCHRRMKHQATCLDIYWTVHPARSLGDIY 127
 DB 17 LSRPLPLEESAMSDCLEAAEQLRNSSLIDCRCHRRMKHQATCLDIYWTVHPARSLGDIY 76
 QY 138 LDVSPYEDVTTSKPKWKNLSKLNMLKPDSDLCCLKFAMLCITLHDKCDRLKAYGEACSGIR 187
 DB 77 LDVSPYEDVTTSKPKWKNLSKLNMLKPDSDLCCLKFAMLCITLHDKCDRLKAYGEACSGIR 136
 QY 188 CORHLCLAQLRSPFFKAEASHAQLLPCAPEDAGCGERRNTIAPSCALPSVTPNCLD 247
 DB 137 CORHLCLAQLRSPFFKAEASHAQLLPCAPEDAGCGERRNTIAPSCALPSVTPNCLD 196
 QY 248 LRSFCRADPLCRSRLMDFQTHCHPMDILGTCAEQSRCLRAYLGLIGTAMTNPFSKVT 307
 DB 197 LRSFCRADPLCRSRLMDFQTHCHPMDILGTCAEQSRCLRAYLGLIGTAMTNPFSKVT 256
 QY 308 TVALSCTCRSGNLODECEQLERSFSQNPCLVEAIAAKWRFHQLFQSDWADSTFSVVOQ 367
 DB 257 TVALSCTCRSGNLODECEQLERSFSQNPCLVEAIAAKWRFHQLFQSDWADSTFSVVOQ 316
 QY 368 QNSNPALRLQPRLPILSILPLILLQTLW 397
 DB 317 QNSNPALRLQPRLPILSILPLILLQTLW 346
 RESULT 12
 ADZ00207
 ID ADZ00207 standard; protein; 346 AA.
 XX AC ADZ00207;
 XX
 DT 30-JUN-2005 (first entry)
 XX
 DE Mouse Ret ligand 3 (RetL3) fragment, SEQ ID NO:15.
 XX
 KW Cell growth; development; signal transduction; neurological disease; renal disease; genitourinary disease; neuroprotective; nephrotropic;
 KW cancer; neoplasm; cytostatic; RetL3;
 KW Ret tyrosine kinase receptor ligand 3; Ret ligand 3;
 KW GDNF family receptor alpha 3; GFR3.
 XX
 OS Mus sp.
 XX
 PN US2005080235-A1.
 XX
 PD 14-APR-2005.
 XX
 PF 23-SEP-2003; 2003US-00668936.
 XX
 PR 08-MAY-1996; 96US-0017427P.
 PR 07-JUN-1996; 96US-0019300P.
 PR 16-JUL-1996; 96US-0021859P.
 PR 23-AUG-1996; 96US-0023444P.
 PR 11-APR-1997; 97US-0043533P.
 PR 07-MAY-1997; 97WO-US007726.
 PR 06-NOV-1998; 98US-00187906.
 XX
 PA (SANI/) SANICOLA-NADEL M.
 PA (HESS/) HESSION C.
 PA (CATE/) CATE R L.
 PA (WORL/) WORLEY D S.
 XX
 PI Sanicola-Nadel M, Hession C, Cate RL, Worley DS;
 XX
 XX WPI; 2005-305025/31.
 DR N-PSDB; ADZ00206.
 XX
 PT New polypeptide sequence that interacts with a receptor protein Ret to trigger dimerization or autophosphorylation, useful in preparing a composition for treating neurodegenerative disorders, e.g., Alzheimer's disease.
 PT
 XX Disclosure; SEQ ID NO 15; 67pp; English.
 PS

XX The invention relates to the murine and human RetL3 (Ret ligand 3)
 CC proteins (AD200209 and AD200213, respectively) and to proteins at least
 CC 80% identical to murine or human RetL3. The invention also discloses
 CC other RetL proteins such as rat RetL1, human RetL1, human RetL2,
 CC fragments of human RetL1, mouse RetL3 and human RetL3, and cDNA sequences
 CC encoding these RetL proteins or protein fragments. Like other RetL
 CC proteins, the RetL3 proteins of the invention interact with the Ret
 CC receptor tyrosine kinase that is encoded by the Ret proto-oncogene,
 CC triggering Ret receptor dimerization or autophosphorylation. The Ret
 CC receptor is expressed during development in a variety of tissues,
 CC including the peripheral and central nervous systems and the kidney. It
 CC is also expressed in some cancers. RetL proteins such as the murine and
 CC human RetL3 proteins, and RetL polynucleotides may be used for
 CC stimulating Ret receptor signaling, thereby promoting renal or neuronal
 CC cell growth or survival and minimizing damage to such tissues after
 CC various insults. They may therefore be used to treat renal disorders
 CC (e.g., renal failure, renal tube defects and renal trauma) or
 CC neurological disorders including neurodegenerative disorders (e.g.,
 CC Alzheimer's disease), bacterial or viral diseases of the nervous system
 CC (e.g., meningitis), neurological damage (e.g. that caused by hemorrhage
 CC or trauma) and developmental neural disorders (e.g., mental retardation).
 CC Conversely, antibodies against RetL may be used to block RetL-Ret
 CC receptor signal transduction for inhibiting tumor growth, fusion proteins
 CC comprising a RetL protein are useful for targeting a drug to Ret receptor
 CC -expressing tumors. Anti-RetL antibodies and RetL fusion proteins may
 CC also be used in medical imaging. The present sequence represents a murine
 CC RetL3 fragment encoded by a murine RetL3 partial cDNA initially
 CC identified by a search of an expressed sequence tag (EST) database using
 CC a rat RetL peptide sequence, and isolated from the EST clones AA049894
 CC and AA050083.

XX Sequence 346 AA;

Query Match 83.2%; Score 1774; DB 9; Length 346;
 Best Local Similarity 100.0%; Pred. No. 1.6e-163;
 Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 68 LSRPLPEESAMADCLAEAEQRLNSLIDCRCHRRMKHQATCLDIYTWVHPARSLGDYE 127
 Db 17 LSRPLPEESAMADCLAEAEQRLNSLIDCRCHRRMKHQATCLDIYTWVHPARSLGDYE 76
 QY 128 LDVSPYEDTTSKPKWKNLSKLNMLKPDSDLCLKFAMLTCLHDKCDRLRKAYGEACSGIR 187
 Db 77 LDVSPYEDTTSKPKWKNLSKLNMLKPDSDLCLKFAMLTCLHDKCDRLRKAYGEACSGIR 136
 QY 188 CORHLCLAQRLRSFFEKAAESHAQGLLLCPAPEDAGCGERRNTIAPSCALPSVTNCLD 247
 Db 137 CORHLCLAQRLRSFFEKAAESHAQGLLLCPAPEDAGCGERRNTIAPSCALPSVTNCLD 196
 QY 248 LRSGFCRADPLCRSLRMDFOQTHCHPMDILGTCAEQSLRAYLGLIGTAMTNPFIKSVNT 307
 Db 197 LRSGFCRADPLCRSLRMDFOQTHCHPMDILGTCAEQSLRAYLGLIGTAMTNPFIKSVNT 256
 QY 308 TVALSTCTCRSGNLQDECEQLERSFSQNPCLVRAIAAKMRFHRLQSFQDWDSTFVSQQ 367
 Db 257 TVALSTCTCRSGNLQDECEQLERSFSQNPCLVRAIAAKMRFHRLQSFQDWDSTFVSQQ 316
 QY 368 QNSNPALRLQPLRPLILSFLPILLOTLW 397
 Db 317 QNSNPALRLQPLRPLILSFLPILLOTLW 346

RESULT 13

AAW65116

ID AAW65116 standard; protein; 400 AA.

XX

AC AAW65116;

XX

DT 28-SEP-1998 (first entry)

XX

DE Human GDNF alpha-3 receptor protein #1.

XX

KW Glial cell line-derived neurotrophic factor alpha-3 receptor; GDNF;
 KW treatment; neurodegenerative disease; Parkinson's Disease; ALS; SMA;
 KW amyotrophic lateral sclerosis; spinal muscular atrophy; nerve; trauma;
 KW Huntington's Disease; Alzheimer's Disease; diabetic neuropathy; muscle;
 KW muscular dystrophy; diagnostic.
 XX Homo sapiens.
 OS
 FH Key Location/Qualifiers
 FT Protein 1..400
 FT /label= GDNF alpha-3
 FT /note= "Partial sequence"
 XX
 PN EP846764-A2.
 PD 10-JUN-1998.
 XX
 PD 20-NOV-1997; 97EP-00309375.
 XX
 PR 27-NOV-1996; 96GB-00024677.
 PR 09-MAY-1997; 97GB-00009463.
 XX
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 XX
 PI Lawrence GMP;
 DR WPI; 1998-299980/27.
 DR N-PSDB; AAV35364.
 XX
 FT New factor alpha 3 receptor polypeptide and e.g. DNA and agonists - used
 FT to treat neuro degenerative diseases, muscular diseases and nerve and
 FT muscle trauma and in diagnostic assays.
 XX
 PS Claim 4; Fig 2; 22pp; English.
 XX
 CC This sequence represents a novel glial cell line-derived neurotrophic
 CC factor alpha-3 receptor (GDNF alpha-3). This protein can be used to treat
 CC e.g. neurodegenerative diseases (such as Parkinson's Disease, amyotrophic
 CC lateral sclerosis (ALS), spinal muscular atrophy (SMA), Huntington's
 CC disease, Alzheimer's Disease, diabetic neuropathy), muscular diseases
 CC (including the muscular dystrophies) and nerve and muscle trauma and in
 CC diagnostic assays for such conditions

SQ Sequence 400 AA;

Query Match 77.3%; Score 1646.5; DB 2; Length 400;
 Best Local Similarity 77.8%; Pred. No. 4.9e-151;
 Matches 305; Conservative 30; Mismatches 56; Indels 1; Gaps 1;
 QY 7 PRPP-LLMILLVLSLWPLGAGNSLATENRFVNSCTQARKKCEANPACKAAYQHLGSGT 65
 Db 9 PLPPVVLMLLLPPSPPLAAGDPLPTESRLMNSCLQARRKQADPTCSAAVHLDST 68
 QY 66 SLSRLPLPEESAMADCLAEAEQRLNSLIDCRCHRRMKHQATCLDIYTWVHPARSLGD 125
 Db 69 SSISTPLPEEESPVPADCLAEAEQRLNSLIDCRCHRRMKHQATCLDIYTWVHPARSLGN 128
 QY 126 YELDVSPYEDTTSKPKWKNLSKLNMLKPDSDLCLKFAMLTCLHDKCDRLRKAYGEACSG 185
 Db 129 YELDVSPYEDTTSKPKWKNLSKLNMLKPDSDLCLKFAMLTCLHDKCDRLRKAYGEACSG 188
 QY 186 IRCQRHLCLAQRLRSFFEKAAESHAQGLLLCPAPEDAGCGERRNTIAPSCALPSVTNPN 245
 Db 189 PHCQRHVCLQLLTTFEKAAPHAQGLLLCPAPEDAGCGERRNTIAPNCALPPVAPNC 248
 QY 246 LDLRSFCRADPLCRSLRMDFOQTHCHPMDILGTCAEQSLRAYLGLIGTAMTNPFIKSV 305
 Db 249 LEILRLCFSDPLCRSLRMDFOQTHCHPMDILGTCAEQSLRAYLGLIGTAMTNPFIKSV 308
 QY 306 NTTVALSTCTCRSGNLQDECEQLERSFSQNPCLVRAIAAKMRFHRLQSFQDWDSTFVSQ 365
 Db 309 NTSVALSTCTCRSGNLQDECEQLERSFSQNPCLVRAIAAKMRFHRLQSFQDWDSTFVSQ 368

QY 366 QOQNSNPALRQPLRPLPILSILPLILLOTW 397
 Db 369 AHQENPAVRPQPWPVPSLSCITLPLILLLSLW 400

RESULT 14
 AAW37463
 ID AAW37463 standard; protein; 400 AA.
 AC AAW37463;
 XX
 XX 21-MAY-1998 (first entry)
 XX
 XX Human Ret ligand RetL3.
 XX
 KW Ret ligand; RetL; RetL3; receptor; signal transduction; human;
 KW cell growth; renal cell; nerve cell; renal failure; nephritis;
 KW kidney transplant; toxic injury; hypoxic injury; neurodegeneration;
 KW motor neurone disease; multiple sclerosis; infection; meningitis;
 KW myelopathy; Creutzfeldt-Jakob disease; cranial nerve injury;
 KW spinal cord injury; Down's syndrome; cerebral palsy; Lyme disease;
 KW muscular dystrophy; myasthenia gravis; tumour; therapy.
 XX
 OS Homo sapiens.
 XX
 XX WO9744356-A2.
 XX
 XX 27-NOV-1997.
 XX
 XX 07-MAY-1997; 97WO-US007726.
 XX
 XX 08-MAY-1996; 96US-0017427P.
 PR 07-JUN-1996; 96US-0019300P.
 PR 16-JUL-1996; 96US-0021859P.
 PR 11-APR-1997; 97US-0043533P.
 XX
 XX (BIOJ) BIOGEN INC.
 PA
 XX
 XX Sanicola-Nadel M, Hession C, Cate RL;
 PI
 XX WPI; 1998-018431/02.
 DR N-PSDB; AAV00251.
 DR
 XX
 XX New nucleic acid encoding ret receptor ligands and related proteins -
 PT vectors, transformed cells and antibodies, used for promoting cell growth
 PT and improving survival of injured cells, especially renal or nerve cells.
 XX
 PS Claim 2; Page 85-86; 113pp; English.
 XX
 XX This amino acid sequence comprises human Ret ligand (RetL) RetL3. Deduced
 CC from cDNA clones (see AAV00251) isolated from a adult heart and spinal
 CC cord libraries. Rat and human RetL1, human RetL2 and mouse RetL3
 CC sequences (see AAW37457-62) are also claimed. Human RetL3 is 34.3%
 CC identical to human RetL1, 34.9% identical to human RetL2 and 76.8%
 CC identical to murine RetL3. Ret ligand is a key component of the Ret
 CC signalling pathway that specifically interacts with Ret receptor protein,
 CC triggering Ret dimerisation and/or autophosphorylation of the Ret.
 CC tyrosine kinase domain. Vectors containing retL3 DNA and prokaryotic or
 CC eukaryotic host cells transformed or transfected with these vectors are
 CC claimed, as well as a method for production of RetL3, its soluble
 CC variants and fusion proteins with a toxin, imageable compound or
 CC radionuclide. RetL3, optionally when expressed from vectors in vivo, is
 CC used to promote growth of new tissue and survival of damaged tissue,
 CC particularly kidney or neural tissue. Typical applications are in renal
 CC failure, nephritis, kidney transplants, toxic or hypoxic injury,
 CC neurodegeneration, motor neurone disease, multiple sclerosis, bacterial,
 CC viral or prion infections (e.g. meningitis, myelopathy associated with
 CC HIV or Creutzfeldt-Jakob disease), cranial nerve or spinal cord injury,
 CC developmental disorders such as Down's syndrome and cerebral palsy, or
 CC conditions involving the peripheral nervous system (Lyme disease,
 CC muscular dystrophy and myasthenia gravis). Fusion proteins are used to
 CC deliver toxins etc. to Ret-expressing cells, especially tumours
 XX

SQ Sequence 400 AA;
 Query Match 77.3%; Score 1646.5; DB 2; Length 400;
 Best Local Similarity 77.8%; Pred. No. 4.9e-151;
 Matches 305; Conservative 30; Mismatches 56; Indels 1; Gaps 1;

QY 7 PRPP-LLMILLVLSLWPLGAGNSLATENRFVNSCTQARKKCEANPACKAAYQHLGSC 65
 Db 9 PLPPVVLMLLLPLPSPPLAAGDPLPTESRLMNSCLQARRKCCQADPTCSAAYHLDSC 68
 QY 66 SLSRPLPLESAMSADCLEAAEQLRNSSLIDCHRRMKHQATCLDIYWTVHPARSLGD 125
 Db 69 SSISTPLPSEEPSVPADCLEAAQQLRNSSLIGCMCHRRMKQVACLDIYWTVHRSLSGN 128
 QY 126 YELDVSPYEDVTTSKPKWNLKLNMLKPDSDCLCKPAMLCITLHDKDRLKAYGEACSG 185
 Db 129 YELDVSPYEDVTTSKPKWNLKLNMLKPDSDCLCKPAMLCITLHDKDRLKAYGEACSG 188
 QY 186 IRCQRHLCLAOQLRSFFKAAESHAQGLLLCPCAPEDAGCGERRRNTIAPSCALPSVTN 245
 Db 189 PHCQRHVCLRQLLTFEKAAPHAQGLLLCPCAPNDRCGERRRNTIAPNCALPPVAPNC 248
 QY 246 LDLRSFCRADPLCRSLMDFTQTHCPMDILGTCAEQSRCLRAYLGLTGTMPTFISKV 305
 Db 249 LELRLCFSDPLCRSLVDFQTHCPMDILGTCAEQSRCLRAYLGLTGTMPTFVSNV 308
 QY 306 NTVVALSCTCRSGNLQDECEQLERSFSQNPCLVEAIAAKMRFHQLFSQDMADSTFVV 365
 Db 309 NTSVALSCTCRSGNLQDECEMLEGFFSHNPCLTEAIAAKMRFHSQDLFSQDMPTTFV 368
 QY 366 QOQNSNPALRQPLRPLPILSILPLILLOTW 397
 Db 369 AHQENPAVRPQPWPVPSLSCITLPLILLLSLW 400

RESULT 15
 AAW84186
 ID AAW84186 standard; protein; 400 AA.
 XX
 AC AAW84186;
 XX
 XX 25-MAR-1999 (first entry)
 XX
 XX Glial cell line-derived neurotrophic factor receptor gamma 2.
 DE
 XX Glial cell line-derived neurotrophic factor receptor gamma 2;
 KW GDNFR-alpha; glial cell line-derived neurotrophic factor; GDNF;
 KW neurodegenerative disease; amyotrophic lateral sclerosis; GDNFR-gamma2;
 KW Parkinson's disease; schizophrenia; insomnia; tardive dyskinesia;
 KW hypertension; pituitary adenomas; hyperprolactinemia; thyroid tumour;
 KW renal disorder; kidney failure; gut dysfunction; regeneration;
 KW cardiomyocyte; epithelium; hepatocyte.
 XX
 OS Homo sapiens.
 FH
 FT Key Location/Qualifiers
 FT Peptide 1..31
 FT Protein /label= signal_peptide
 FT Domain 32..400
 FT Domain /label= mature_protein
 FT Domain 32..382
 FT Domain /note= "extracellular domain"
 FT Domain 383..400
 FT Domain /note= "transmembrane domain"
 XX
 XX WO9853069-A2.
 XX
 XX 26-NOV-1998.
 XX
 XX 20-MAY-1998; 98WO-US010328.
 XX
 XX 20-MAY-1997; 97US-0047092P.
 XX 27-JUN-1997; 97US-00884638.
 PR

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